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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model
Run on: June 15, 2003, 13:28:23 ; Search time 1:35.75 Seconds
(without alignments)
10479.665 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517

Sequence: 1 ggacggagacgtctcgcg.....tgaatacacaagaat 517

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

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2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ovr:*

6: gb_pat:*

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9: gb_pr:*

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11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

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34: em_htg_pln:*

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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

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2 AX147742	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
3 AX147742.1	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
4 GI:14346787	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
5 AX147742	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
6 AX300791	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
7 HSIGF1A	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
8 HSIGF1B	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
9 HSIGF1C	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
10 HSIGF1D	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
11 HSIGF1E	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
12 HSIGF1F	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
13 HSIGF1G	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
14 HSIGF1H	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
15 HSIGF1I	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
16 HSIGF1J	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
17 HSIGF1K	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
18 HSIGF1L	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
19 HSIGF1M	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
20 HSIGF1N	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
21 HSIGF1O	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
22 HSIGF1P	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
23 HSIGF1Q	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
24 HSIGF1R	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
25 HSIGF1S	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
26 HSIGF1T	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
27 HSIGF1U	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
28 HSIGF1V	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
29 HSIGF1W	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
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35 HSIGF1AC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
36 HSIGF1AD	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
37 HSIGF1AE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
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41 HSIGF1AI	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
42 HSIGF1AJ	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
43 HSIGF1AK	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
44 HSIGF1AL	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.
45 HSIGF1AM	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Sequence 1 from Patent WO0136483.

ALIGNMENTS

REFERENCE 1 (bases 1 to 517)
AUTORS Goldspink,G.R. and Johnson,I.R.
TITLE Use of the insulin-like-growth factor isoform mgf for the treatment of neurological disorders

JOURNAL	Patent: WO 0136483-A 1 25-MAY-2001;	University College London (GB)	; East Grinstead Medical Research
FEATURES	source	Location/Qualifiers	1..517
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ORIGIN		BASE COUNT	150 a 130 c 139 g 98 t
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Db	61 AGGGCTTTATTCAACAGGCCACAGGTATGCTCCAGACTCGAGGGGCCCTAG 120	Db	61 AGGGCTTTATTCAACAGGCCACAGGTATGCTCCAGACTCGAGGGGCCCTAG 120
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Db	121 ACAGGATCGGGATGAGTGGCTCCGGAGCTGATCTAAGGGGTGAGATGT 180	Db	121 ACAGGATCGGGATGAGTGGCTCCGGAGCTGATCTAAGGGGTGAGATGT 180
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Db	181 TCGCACCCCTCAAGCTGCCAAGTCAGCTGGCTCGTCCGGAGGCCACCGAC 240	Db	181 TCGCACCCCTCAAGCTGCCAAGTCAGCTGGCTCGTCCGGAGGCCACCGAC 240
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Qy	361 GATGTAGAGACCTCTGAGAGTGAAAGAGGACAGGCCACCGCAGGCCACCGC 420	Qy	361 GATGTAGAGACCTCTGAGAGTGAAAGAGGACAGGCCACCGCAGGCCACCGC 420
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Qy	481 GATGGATTCCCCCATGAATAACAGTAACT 517	Qy	481 GATGGATTCCCCCATGAATAACAGTAACT 517
Db	481 GATGGATTCCCCCATGAATAACAGTAACT 517	Db	481 GATGGATTCCCCCATGAATAACAGTAACT 517
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LOCUS	AX300779	LOCUS	AX147746
DEFINITION	Sequence 1 from Patent WO0185781.	DEFINITION	Sequence 5 from Patent WO136483.
VERSION	AX300779.1	VERSION	AX147746.1
ACCESSION	GT:17382060	ACCESSION	GT:14346791
KEYWORDS		KEYWORDS	
SOURCE	human	ORGANISM	Oryctolagus cuniculus
ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 Goldspink, G.B. and Terenghi, G.B.	REFERENCE	1 (bases 1 to 523) Goldspink, G.R. and Johnson, I.R.
AUTHORS		AUTHORS	Use of nerve damage
TITLE		TITLE	treatment of neurological disorders
JOURNAL	Patent: Wo 0185781-A 1 15-NOV-2001;		

JOURNAL	Patent: WO 0136483 A5 25-MAY-2001; University College London (GB)				
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ORIGIN	ORIGIN				
Query Match	90.4%; Score 467.4; DB 6; Length 523;				
Best Local Similarity	96.2%; Pred. No. 4.8e-139; Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;				
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Db	181 TGCACACCTCAGGCCAGTCAGCTCGCTCTGCGGCCAGGCCACCGAC 240 181 TGCACACCTCAGGCCAGTCAGCTCGCTCTGCGGCCAGGCCACCGAC 240				
Qy	241 ATGCCAAGACCTCAAGCTCAGAGTATGAGCTCACTTACCAACAGAAATGAGTCAGAG 297 241 ATGCCAAGACCTCAAGCTCAGAGTATGAGCTCACTTACCAACAGAAATGAGTCAGAG 297				
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Db	417 CTCTGACAGTACCTGAAACATTGGATACGGCCAAATAAATAGTTGACATT 476 421 CTCTGACAGTACCTGAAACATTGGATACGGCCAAATAAATAGTTGACATT 480				
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LOCUS	Sequence 5 from Patent WO0185781.				
DEFINITION	AX300783.1 GI:17382064				
VERSION	1				
KEYWORDS	rabbit.				
SOURCE	Oryctolagus cuniculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
REFERENCE	1 Goldspink,G.D. and Terenghi,G.B.				
AUTHORS	Repair of nerve damage				
TITLE	Patent: WO 0185781-A5 15-NOV-2001;				
JOURNAL	treatment of neurological disorders				
RESULT 4	RESULT 5				
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LOCUS	AX147754				
DEFINITION	Sequence 13 from Patent WO0136483.				
ACCESSION	AX147754				
VERSION	AX147754.1 GI:1348552				
KEYWORDS	rabbit.				
SOURCE	Oryctolagus cuniculus				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.				
REFERENCE	1 (bases 1 to 471)				
AUTHORS	Goldspink,G. and Johnson,I.R.				
TITLE	Use of the insulin-like-growth factor i isoform mfg for the				
JOURNAL	treatment of neurological disorders				

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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
 AUTHORS Baak,J. and Mutter,G.L.
 TITLE Prognostic classification of breast cancer
 JOURNAL THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; Baak, Jan (US)
 FEATURES source
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 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

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 DEFINITION ACCESSION X57025
 VERSION X57025.1 GI:33007
 KEYWORDS insulin-like growth factor I.
 SOURCE Homo sapiens.
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE AUTHORS Steenbergh,P.H.
 TITLE Submitted (18-DEC-1990) P.H. Steenbergh, LAB FOR PHYSIOLOGICAL
 JOURNAL CHEMISTRY, UNIVERSITY OF UTRECHT, VONDELLAAN 24 A, 3521 GG Utrecht,
 THE NETHERLANDS
 REFERENCE AUTHORS Steenbergh,P.H., Kooij-Reemst,A.M., Cleutjens,C.B. and
 Sussebach,J.S.
 TITLE Complete nucleotide sequence of the high molecular weight human
 IGF-I mRNA
 JOURNAL Biochem. Biophys. Res. Commun. 175 (2), 507-514 (1991)
 MEDLINE 91207342
 PUBMED 2018498
 FEATURES source
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BASE COUNT 2330 a 1415 c 1240 g 2275 t
 ORIGIN Query Match 66.6%; Score 344.7; DB 9; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 3.4e-99; Mismatches 13; Indels 53; Gaps 5;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;
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 Db 622 GATGTTAGAGACCTCTGTGAGAGTGAGAGTGCACGCCAGGACATCTTGCTC 681
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 QY 420 TGGAC-ATTACCTG-TAACATTGGATAACGGCCAAATAAGTTGATCACATTTC 477
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FEATURES	source	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Location/Qualifiers						
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Best Local Similarity		87.1%	Pred. No. 7.9e-99;					
Matches		454;	Conservative 0;	Mismatches 14;	Indels 5;	Gaps 5;		
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Db	67	GGACCGAGAGCTCTGGGGCTGAGCTSGTGTGAGCTCTCGTGTGAGAC	67					
Db	127	AGGGCTTATTCAACAAGCCACAGGTATGGCCAGCAGTGGAGGGGCCCTAG	126					
QY	61	AGGGCTTATTCAACAAGCCACAGGTATGGCCAGCAGTGGAGGGGCCCTAG	120					
Db	121	ACGGCATCGTGGATGAGTCGCTTCCGGAGCTGGATCTAAGGGCTGGAGATGAT	180					
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QY	181	TSGCACCCCTAACGGCTGGAGCTGGATCTAAGGGCTGGAGATGCTCTCGTGTGCTGGAGAC	240					
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QY	241	ATGCCAGACCCAGAGTAACTACAGCCACAGACAGACAGAAGCTCTCGAGA	300					
Db	307	ATGCCAGACCCAGAGTAACTACAGCCACAGACAGACAGAAGCTCTCGAGA	321					
QY	301	AGGAAGGAGTACATTGAGAACAGAACAGTAGAGGAGTGAGGAGACAGACAG	360					
Db	322	---AAGGAAGTACATTGAGAACAGAACAGTAGAGGAGTGAGGAGACACTACAG	377					
QY	361	GATGTA-GAAGACCTCTGAGGAGTGAAGAACAGAACAGAACAGAACACTACAG	419					
Db	378	GATGAGGAGACCCCTGAGGAGTGAAGAACAGAACAGAACAGAACACTACAG	437					
QY	420	TGAC-AGT-TACCTG-TAACATGATAACGGCAAATTAAGTTGATCACATTTC	477					
Db	438	TGGAGGAGTACCTGTAACCTACACCTACACCAAAATAGTTGATAACATTA	497					
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QY	1	GGACCGAGACCTCCCGGGCTGACTGGATGCTCTCACTCGCTGTGGAGAC	60					
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QY	301	AGGAAGGAGTACATTGAGAACAGAACAGTAGAGGAGTGAGGAGACAGACAG	360					
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Db	378	GATGAGGAGACCCCTGAGGAGTGAAGAACAGAACAGAACAGAACACTACAG	437					
QY	420	TGAC-AGT-TACCTG-TAACATGATAACGGCAAATTAAGTTGATCACATTTC	477					
Db	438	TGGAGGAGTACCTGTAACCTACACCTACACCAAAATAGTTGATAACATTA	497					
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QY	181	TSGCACCCCTAACGGCTGGAGCTGGATCTAAGGGCTGGAGATGCTCTCGTGTGCTGGAGAC	240					
Db	247	TGCACCCCTAACGGCTGGAGCTGGATCTAAGGGCTGGAGATGCTCTCGTGTGCTGGAGAC	306					
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Db	307	ATGCCAGACCCAGAGTAACTACAGCCACAGACAGACAGAAGCTCTCGAGA	321					
QY	301	AGGAAGGAGTACATTGAGAACAGAACAGTAGAGGAGTGAGGAGACAGACAG	360					
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QY	478	AAGAT-GCATTCCTCCAAATGAAATACACAGTAACAT 517						
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QY	1	GGACCGAGACCTCCCGGGCTGACTGGATGCTCTCACTCGCTGTGGAGAC	60					
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RESULT 14

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 ACCESSION M29644
 VERSION M29644.1 GI:183119
 KEYWORDS Insulin-like growth factor
 SOURCE Human (adult) liver, cDNA to mRNA.
 ORGANISM Homo sapiens

REFERENCE Rall,L.B., Scott,J. and Bell,G.I.
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 JOURNAL Mammalia; Butcheria; Primates; Catarrhini; Hominidae; Homo.
 MEDLINE 88665102
 PUBMED 3683205

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 Db 527 TGCAGCAGTACCTGTAACTTGTGAACACTACCAACAAATAGTTGATACATTA 586

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 Db 587 AAAGATGGGTTTCCCCAAATGAAATCACAGTAACAT 627

RESULT 15

LOCUS HUMIGFII 1076 bp mRNA linear PRI 08-NOV-1994
 DEFINITION Human insulin-like growth factor mRNA, complete cds.
 ACCESSION M27544
 VERSION M27544.1 GI:184829
 KEYWORDS Insulin-like growth factor.
 SOURCE Human liver, cDNA to mRNA, clones lambda-TG[03,04,05].

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1076)
 AUTHORS Le Bouc,Y., Dreyer,F., Jaeger,F., Binoux,M. and Sondermeyer,P.
 TITLE Complete characterization of the human IGF-I nucleotide sequence isolated from a newly constructed adult liver cDNA library
 JOURNAL FEBS Lett. 196 (1), 108-112 (1986)
 MEDLINE 8610910
 PUBMED 2935423

FEATURES

source Location/Qualifiers

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sig-peptide

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Query Match 66.3%; Score 342.6; DB 9; Length 1076;

Best Local Similarity 87.1%; Pred. No. 8.5e-99;
 Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

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Qy	61	GGCTTTTATTACAAAGCCACAGSSTATGCTCAGACTGGAGGCCTAG	120
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Qy	361	GATGTA-GAACACCCCTCTGAGACTGAAAGGAGCAGGCCACCGACCCCTTGCTC	419
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 Job time : 1439.75 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model
Run on: June 15, 2003, 09:07:57 : Search time 156.835 Seconds
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Gapcp 10.0 , Gapext 1.0
Searched: 2185239 seqs, 1125999159 residues
Total number of hits satisfying chosen parameters: 4370478
Minimum DB seq length: 0
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Post-processing: Minimum Match: 0%
Maximum Match: 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
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2	517	100	0	AAS16877 Human mechano-grow
3	467.4	90	4	22 AAD6400 Rabbit IgF-I isofo
4	467.4	90	4	523 22 AAD6400 Rabbit mechano-grow
5	467.4	90	4	523 22 AAD6400 Rabbit insulin lik
6	377.2	73	0	18 AAS16893 Rabbit insulin-type
7	377.2	471	24	22 AAD6405 Rabbit insulin-like
8	344.2	66	6	8 AAS16884 Sequence encoding
	-818	-	-	RANT0435

SUMMARIES

PI	Goldspink G, Johnson I;	XX	15-NOV-2000; 2000WO-GB04354.	Db	421 GCGACAGTTACCTGTAACATGGATAACGGCCAAAATAGTTGATCACATTCAA	480
XX	DR	PR	15-NOV-1999; 99GB-0026968.	Qy	481 GATGGCATTCCCCATGAAATACAAGTAAC	517
XX	(UNILO) UNIV COLLEGE LONDON.	PA		Ps	GATGSCATTCCCCATGAAATACAAGTAAC	517
XX	Goldspink G, Johnson I;	XX		Db	481 GATGGCATTCCCCATGAAATACAAGTAAC	517
DR	WPI: 2001-355620/37.	P-PSDB; AAI02447.				
XX	Use of mechano-growth factor, an isoform of insulin-like Growth Factor-I, capable of reducing motoneurone loss, in the manufacture of a medicament for the treatment of neurological disorder -	PT				
XX	Claim 4: Page 49-50; 66pp; English.	PS				
XX	The present invention relates to use of mechano-growth factor (Mgf), an insulin-like growth Factor-I (IGF-I) isoform in the manufacture of a medicament for the treatment of neurological disorder. The Mgf is capable of reducing motoneurone loss by 20% or greater in response to nerve avulsion, and effects motoneurone rescue. The Mgf polypeptide and polypeptide are useful in the manufacture of a medicament for the treatment of a neurological disorder, including a disorder of motoneurones and/or neurodegenerative disorder, e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive spinal muscular atrophy, infantile or juvenile muscular atrophy, progressive polyradiculitis or post-polio syndrome, a disorder caused by exposure to a toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an injury that affects motoneurones, motoneurone loss associated with aging, autosomal or sex-linked muscular dystrophy, diabetic neuropathy, peripheral neuropathies, Alzheimer's disease and Parkinson's disease. The present sequence is human IGF-I isoform Mgf cDNA. Mgf is a muscle isoform having extracellular (Ec) domain, hence also referred as IGF-I-Ec. The Mgf protein comprises amino acid sequences encoded by nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame of Mgf.	CC				
XX	Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;	SQ				
Query Match	100.0%; Score 517; DB 22; Length 517;					
Best Local Similarity	100.0%; Pred. No. 2e-146;					
Matches	517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
Oy	1 GGACGGGAGACSTCTCGGSGCTGAGTCGTTCTCAGTCGTTGAGAC	60	Key	Location/Qualifiers		
Dy	1 GGACGGGAGACGCTCTGGGGGTGAGCTGTTGATGCTCTCAGTGTGAGAC	60	FH	1..333		
Oy	61 AGGGCTTTATCAAGGCCAACGGTAGGCTCAGCAGTCAGGAGGGCTCAG	120	FT	/*tag= a		
Dy	61 AGGGCTTTATCAAGGCCAACGGTAGGCTCAGCAGTCAGGAGGGCTCAG	120	FT	/product= "Human Mgf"		
Oy	121 ACAGGATCTGGATGAGTCCTCCGGAGCTGTTGAGATGTA	180	FT	/partial		
Dy	121 ACAGGATCTGGATGAGTCCTCCGGAGCTGTTGAGATGTA	180	FT	/note= "No start codon"		
Oy	181 TGCGCACCTCAGGCCAACGGCTCAGTCAGTCAGGAGGTGAGATGTA	300	FT	1..76		
Dy	181 TGCGCACCTCAGGCCAACGGCTCAGTCAGTCAGGAGGTGAGATGTA	300	FT	/*tag= b		
Oy	241 ATGCCAAGGCCAGAACGAACTACGCCCATCTACCAACAAAGCACCAAGTCTCAGGA	360	FT	/number= 3		
Dy	241 ATGCCAAGGCCAGAACGAACTACGCCCATCTACCAACAAAGCACCAAGTCTCAGGA	360	FT	77..259		
Oy	361 GATGAGAGACCTCTGAGGAGACACAGTAGAGGGAGTGAGGAACAAAGACTACAG	420	FT	/*tag= c		
Dy	361 GATGAGAGACCTCTGAGGAGACACAGTAGAGGGAGTGAGGAACAAAGACTACAG	420	FT	/number= 4		
Oy	301 AGGAAAGAAAGTCTTGAAGAACACAGTAGAGGGAGTGAGGAACAAAGACTACAG	360	FT	260..307		
Dy	301 AGGAAAGAAAGTCTTGAAGAACACAGTAGAGGGAGTGAGGAACAAAGACTACAG	360	FT	/*tag= d		
Oy	361 GATGAGAGACCTCTGAGGAGACACAGTAGAGGGAGTGAGGAACAAAGACTACAG	420	FT	/number= 5		
Dy	361 GATGAGAGACCTCTGAGGAGACACAGTAGAGGGAGTGAGGAACAAAGACTACAG	420	FT	308..330		
Oy	301 AGGAAAGAAAGTCTTGAAGAACACAGTAGAGGGAGTGAGGAACAAAGACTACAG	360	FT	/*tag= e		
Dy	301 AGGAAAGAAAGTCTTGAAGAACACAGTAGAGGGAGTGAGGAACAAAGACTACAG	360	FT	/number= 6		
Oy	361 GATGAGAGACCTCTGAGGAGACACAGTAGAGGGAGTGAGGAACAAAGACTACAG	420	PN	WO200185781-A2.		
Dy	361 GATGAGAGACCTCTGAGGAGACACAGTAGAGGGAGTGAGGAACAAAGACTACAG	420	PD	15-NOV-2001.		
Oy	10-MAY-2001; 2001WO-GB02054.	XX	PP	10-MAY-2001; 2000GB-0011278.		
Dy	10-MAY-2001; 2001WO-GB02054.	XX	PR			
Oy	(UNILO) UNIV COLLEGE LONDON.	PA	PA	(UNILO) EAST GRINSTEAD MEDICAL RES TRUST.		
Dy	(UNILO) EAST GRINSTEAD MEDICAL RES TRUST.	XX	PA			
Oy	Goldspink G, Terenghi G;	XX	PI			
Dy	WPI: 2002-05585/07.	DR	DR			
Oy	P-PSDB; AAI0559.	XX	Ps			
Dy	Ps	XX	PT			
Oy	Use of insulin-like growth factor I (IGF-I) isoform known as mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has ability to reduce motoneuron loss in response to nerve avulsion, to treat nerve damage.	PT	PT			
Dy	Claim 11; Fig 5; 65pp; English.	XX	PT			
Oy	The invention relates to the use of an insulin-like growth factor I (IGF-I) isoform, known as mechano-growth factor (Mgf), in the manufacture of a medicament for treating nerve damage in the peripheral nervous system, or for treating nerve damage by localising Mgf at the site of damage. The nerve damage may include severing of a nerve. The treatment may be combined with another treatment (such as a polypeptide growth	CC	CC			

CC factor other than MGF) that prevents or diminishes degeneration of the target organ (for example, muscle) which the damaged nerve innervates; CC whereby the treatment of the muscle with MGF or a polynucleotide encoding CC MGF prevents or diminishes degeneration. The method is useful for CC treating neurological disorders, preferably motorneuron disorders. These methods can reduce motorneuron loss by 20% or greater in response to nerve avulsion. This sequence represents cDNA encoding the human MGF.

XX Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 100.0%; Score 517; DB 24; Length 517;

Best Local Similarity 100.0%; Pred. No. 2e-146; Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GACCGGAGACGCCTGGGGCTGAGCTGGTGTGATGCTCTCAGTCGTTGAGCTGAGCTGAGCTGCTCTCACTGATGCTGTTGAGAC 60

QY 61 AGGGCTTATTTCAGCAGGCCACAGGTAGGCTCAGAGTCGAGGTCGAGGCGCCCTCAG 120

Db 61 AGGGCTTATTTCAGCAGGCCACAGGTAGGCTCAGAGTCGAGGTCGAGGCGCCCTCAG 120

QY 121 ACAGGCATGGTAGTGCTTCGGAGCTGGATCTAGAGGCTGGAGAT 180

Db 121 ACAGGCATGGTAGTGCTTCGGAGCTGGATCTAGAGGCTGGAGAT 180

QY 181 TGCCACCCCTCAAGCTGCCCAGTCAGTCCTGCGGCGCCACACCGAC 240

Db 241 ATGCCAACAGACCCAGAACTACCCACCATCACACAGAACAGAGCTCAGAGA 300

QY 301 AGGAAAGGAATGATGAAAGACACAGTAAGGAGGTGAGGAACAACTACAG 360

Db 301 AGGAAAGGAATGATGAAAGACACAGTAAGGAGGTGAGGAACAACTACAG 360

QY 361 GATGTTAGAGAACCTTCGAGGAGTGAAGAACAGCCACCGCAGACCTTGTCT 420

Db 361 GATGTTAGAGAACCTTCGAGGAGTGAAGAACAGCCACCGCAGACCTTGTCT 420

QY 421 GCACAGTTACCTGAAATGATGAAATGGATACCGGAAATAATAGTTGATCACATTCAA 480

Db 421 GCACAGTTACCTGAAATGATGAAATGGATACCGGAAATAATAGTTGATCACATTCAA 480

QY 481 GATGCCATTCCCCAATGAAATCACAGTAACAT 517

Db 481 GATGCCATTCCCCAATGAAATCACAGTAACAT 517

Query Match 100.0%; Score 517; DB 24; Length 517;

Best Local Similarity 100.0%; Pred. No. 2e-146; Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 GACCGGAGACGCCTGGGGCTGAGCTGGTGTGATGCTCTCAGTCGTTGAGCTGAGCTGCTCTCACTGATGCTGTTGAGAC 60

QY 61 AGGGCTTATTTCAGCAGGCCACAGGTAGGCTCAGAGTCGAGGTCGAGGCGCCCTCAG 120

Db 61 AGGGCTTATTTCAGCAGGCCACAGGTAGGCTCAGAGTCGAGGTCGAGGCGCCCTCAG 120

QY 121 ACAGGCATGGTAGTGCTTCGGAGCTGGATCTAGAGGCTGGAGAT 180

Db 121 ACAGGCATGGTAGTGCTTCGGAGCTGGATCTAGAGGCTGGAGAT 180

QY 181 TGCCACCCCTCAAGCCGCAAGGAGCCAGTCAGTCGCTGCTGGCCAGGCCACACCGAC 240

Db 181 TGCCACCCCTCAAGCCGCAAGGAGCCAGTCAGTCGCTGCTGGCCAGGCCACACCGAC 240

QY 241 ATGCCAACAGACCCAGAACTACCCACCATCACACAGAACAGCTGAGTCAGAGG 297

Db 241 ATGCCAACAGACCCAGAACTACCCACCATCACACAGAACAGCTGAGTCAGAGG 300

FT /*tag= a
FT /product= "Mechano-growth factor (MGF)"
FT //note= "This region comprises exons 3-6. The CDS does
FT not include start codon"
FT /partial

PN WO200136483-A1.
XX 25-MAY-2001.
PR 15-NOV-1999; 99GB-0026968.
PA (UNLO) UNTV COLLEGE LONDON.
PT Goldsbink G, Johnson I;
DR DR
DR DR
XX WPI; 2001-3556/0-37.
PT PT-PSDB; AAE02449.

PT Use-of mechano-growth factor, an isoform of Insulin-like Growth Factor-I, capable of reducing motoneurone loss, in the manufacture of a medicament for the treatment of neurological disorder -
PT XX
PS Claim 4; Page 53-54; 66pp; English.
XX
CC The present invention relates to use-of mechano-growth factor (MGF) of
CC an Insulin like Growth Factor-I (IGF-I) isoform in the manufacture of a
CC medicament for the treatment of neurological disorder. The MGF is capable
CC of reducing motoneurone loss by 20% or greater in response to nerve
CC avulsion, and effects motoneurone rescue, preferably adult motoneurone
CC rescue. The MGF Polynucleotide and polypeptide are useful in the
CC manufacture of a medicament for the treatment of a neurological disorder,
CC including a disorder of motoneurones and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinobulbar or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC injury that affects motoneurones, motoneurone loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
CC isoform having extracellular (Ec) domain, hence also referred as
IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
CC of MGF.
XX

Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 90.4%; Score 467.4; DB 22; Length 523;

Best Local Similarity 96.2%; Pred. No. 2.1e-131; Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Db 1 GGACCGGAGAGCTCGGGGGCTAGCTGGTGGATGCTCTCACTGGGGGGCTCAG 50

QY 61 AGGGCTTATTTCAGCAGGCCACAGGTAGGCTCAGTCGCTGCTGGCCAGGCCACACCGAC 120

Db 61 AGGGCTTATTTCAGCAGGCCACAGGTAGGCTCAGTCGCTGCTGGCCAGGCCACACCGAC 120

QY 121 ACAGGCATGGTAGTGCTTCGGAGCTGGATCTAGAGGCTGGAGAT 180

Db 121 ACAGGCATGGTAGTGCTTCGGAGCTGGATCTAGAGGCTGGAGAT 180

QY 181 TGCCACCCCTCAAGCCGCAAGGAGCCAGTCAGTCGCTGCTGGCCAGGCCACACCGAC 240

Db 181 TGCCACCCCTCAAGCCGCAAGGAGCCAGTCAGTCGCTGCTGGCCAGGCCACACCGAC 240

QY 241 ATGCCAACAGACCCAGAACTACCCACCATCACACAGAACAGCTGAGTCAGAGG 297

Db 241 ATGCCAACAGACCCAGAACTACCCACCATCACACAGAACAGCTGAGTCAGAGG 300

RESULT 3

AA006400 Best Local Similarity 96.2%; Pred. No. 2.1e-131; Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

ID AA006400 standard; cDNA; 523 BP.

XX AC 10-AUG-2001 (first entry)

DE Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.

XX DE Rabbit IGF-I isoform mechano-growth factor (MGF);

KW mechano-growth factor; neurodegenerative disorder;

KW amytrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

KW polyneuropathy; post-polio syndrome; toxin; motoneurone disorder;

KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;

KW sex-linked muscular dystrophy; peripheral neuropathy;

KW Alzheimer's disease; Parkinson's disease; ss.

XX OS Oryctolagus cuniculus.

XX OS Key location/Qualifiers

FT CDS 1..336

QY 298 AGNAGGAAAGAAGTACATTGAGAACACAGTAGGGGTGAGGAACAGAACTA 357
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 301 AGAGGAAAGAAGTACATTGAGAACACAGTAGGGGTGAGGAACAGAACTA 360
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 358 CAGGATGA-GAGACCTTGAGAGTGGAGTGGAGAAGGACGCCACGGACCTTG 416
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 361 CAGGATGAGACCTTGAGAGTGGAGTGGAGAAGGACGCCACGGACCTTG 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 417 CTCTGCAGTACTGTAACATGGATCCGGCAAAATAATAGTTGATCACATT 476
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 421 CTCTGCAGTACTGTAACATGGATCCGGCAAAATAATAGTTGATCACATT 480
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 477 CAAGATGCAATTCCCCCATGAAATACACAGTACAT 517
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 481 CAAGATGCAATTCCCCCATGAAATACACAGTACAT 521

RESULT 4

AAS16879
 ID AAS16879 standard; cDNA; 523 BP.
 XX
 AC AAS16879;
 XX
 DT 25-FEB-2002 (first entry)
 DE Rabbit mechano-growth factor (MGF) cDNA.
 XX
 KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF; neuroprotective; nerve damage; peripheral nervous system; nerve severing; muscle; neurological disorder; motoneuron loss; motorneuron disorder; ss; nerve avulsion.

OS Oryctolagus cuniculus.

PH Key Location/qualifiers

CD5 1.336 /*tag= a "Rabbit MGF"
 /product= "Rabbit MGF"
 /partial=
 /note= "No start codon"
 1..76 /*tag= b
 /number= 3
 77..259 /*tag= c
 /number= 4
 260..309 /*tag= d
 /number= 5
 311..333 /*tag= e
 /number= 6

FT exon
 PR WO200185781-A2.
 PR 15-NOV-2001.
 PR 10-MAY-2001; 2001WO-GB02054.
 PR 10-MAY-2000; 2000GB-0011278.
 PR XX
 PA (UNILO) UNIV COLLEGE LONDON.
 PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
 XX
 PI Goldspink G, Teyerghi G;
 XX
 DR WPI; 2002-055585/07.
 DR P-PSDB; AAT010561.

PT treat nerve damage
 XX Disclosure: Fig 7; 65pp; English.

CC The invention relates to the use of an insulin-like growth factor I (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture of a medicament, for treating nerve damage in the peripheral nervous system, or for treating nerve damage by localising MGF at the site of damage. The nerve damage may include severing of a nerve. The treatment may be combined with another treatment (such as a polypeptide growth factor other than MGF) that prevents or diminishes degeneration of the target organ (for example, muscle) which the damaged nerve innervates, whereby the treatment of the muscle with MGF or a polynucleotide encoding MGF prevents or diminishes degeneration. The method is useful for treating neurological disorders, preferably motorneuron disorders. These methods can reduce motoneuron loss by 20% or greater in response to nerve avulsion. This sequence represents cDNA encoding the rabbit MGF.

SQ Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 90.4%; Score 467.4; DB 24; Length 523;
 Best Local Similarity 96.2%; Pred. No. 2.1e-131;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

Db 1 GGACGGAGGCTGTGGGGCTGAGCTGGTGTGTTCTCAGTGCTGGTGAGAC 50
 QY 1 GGACGGAGGCTGTGGGGCTGAGCTGGTGTGTTCTCAGTGCTGGTGAGAC 60

Db 61 AGGGCTTTATTCAACAGGCCACAGGTGATGGTCAGCAGTCGGAGGGCTCG 120
 QY 61 AGGGCTTTATTCAACAGGCCACAGGTGATGGTCAGCAGTCGGAGGGCTCG 120

Db 121 ACAGGCATCTGTGAGGAGTGCTGCTGGTGGAGATGTAC 180
 QY 121 ACAGGCATCTGTGAGGAGTGCTGCTGGTGGAGATGTAC 180

Db 181 TGCGCACCCCTCAAGCGGAAAGCGACGCCGCTCGCTGGTGGAGATGTAC 240
 QY 181 TGCGCACCCCTCAAGCGGAAAGCGACGCCGCTCGCTGGTGGAGATGTAC 240

Db 241 ATGCCAAGACCCAGGTACATGCCCTCACTTACACAGAACACAGTCTCA - - G 297
 QY 241 ATGCCAAGACCCAGGTACATGCCCTCACTTACACAGAACACAGTCTCA - - G 297

Db 241 ATGCCAAGACCCAGGTACATGCCCTCACTTACACAGAACACAGTCTCA 300
 QY 241 ATGCCAAGACCCAGGTACATGCCCTCACTTACACAGAACACAGTCTCA 300

Db 298 AGAAGGAAAGAAGTACATTGAGAACACAAGTAGAGGAGGAGGAGGAGA 357
 QY 298 AGAAGGAAAGAAGTACATTGAGAACACAAGTAGAGGAGGAGGAGGAGA 357

Db 301 AGAAGGAAAGAAGTACATTGAGAACACAAGTAGAGGAGGAGGAGGAGA 360
 QY 358 CAGGATGA-GAGACCTTGAGAGTGGAGTGGAGAAGGACGCCACGGACCTTG 416
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 361 CAGGATGAGACCTTGAGAGTGGAGTGGAGAAGGACGCCACGGACCTTG 420
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 417 CTCTGCAGTACTGTAACATGGATCCGGCAAAATAATAGTTGATCACATT 476
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 421 CTCTGCAGTACTGTAACATGGATCCGGCAAAATAATAGTTGATCACATT 480
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 477 CAAGATGCAATTCCCCCATGAAATACACAGTACAT 517
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 481 CAAGATGCAATTCCCCCATGAAATACACAGTACAT 521

RESULT 5

AAT84893
 ID AAT84893 standard; cDNA; 553 BP.
 XX
 AC AAT84893;
 XX
 DT 14-APR-1998 (first entry)
 XX DE Rabbit insulin like growth factor 1
 XX Insulin like growth factor 1; IGF-I; Ec peptide; muscle disorder;
 KW heart; neuromuscular disease; primer; ss.

Use of insulin-like growth factor I (IGF-I) isoform known as mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has ability to reduce motoneuron loss in response to nerve avulsion, to

XX	OS	oryctolagus cuniculus.
XX	FH	Location/Qualifiers
Key	1: 366	
CDS	/*tag= a	
FT	/product= "IGF-1"	
FT		
XX	PR	WO9733997-A1.
XX	PD	18-SEP-1997.
XX	PF	11-MAR-1997; 97WO-GB00658.
XX	PR	11-MAR-1996; 96GB-0005124.
XX	PA	(UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
XX	PI	Goldspink G;
XX	DR	WPI; 1997-470877/43.
XX	P-PSDB	AAW23301.
XX	PT	Use of insulin like growth factor I characterised by presence of EC peptide - to treat humans or animals, particularly muscle disorders, heart conditions or neuromuscular diseases
XX	PT	Disclosure; Fig 3; 33pp; English.
XX	CC	A use of insulin like growth factor I (IGF-1) has been developed, and is characterised by the presence of the EC peptide, or a functional equivalent, in the treatment or therapy of a human or animal. The IGF-1 polypeptide can be used to treat muscular disorders, e.g. Duchenne or Becker muscular dystrophy, autosomal dystrophies and related progressive skeletal muscle weakness and wasting, muscle atrophy in ageing humans, spinal cord injury induced muscle atrophy and neuromuscular diseases, and cardiac disorders, e.g. diseases where promotion of cardiac muscle protein synthesis is a beneficial treatment, cardiomyopathies and acute heart failure or insult, specifically myocarditis or myocardial infarction. It can also be used to promote bone fracture healing and maintenance of bone in old age. The present sequence encodes rabbit IGF-1 used in the present specification.
XX	SQ	Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;
QY	Query Match	90.4%; Score 467.4; DB 18; Length 553;
QY	Best Local Similarity	96.2%; Pred. No. 2.1e-131;
QY	Matches	501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;
QY	1	GGACGGGAGACGCCCTGGGGCTGGTGGATGCTCTCAGTCAGTGCTGGAGAC
Db	31	GGACCGAGAGCCTGGCTGGCTGGAGCTGCTTGTGAGAC
QY	61	AGGCTTTATTCACAGCCACAGGTGCTAGGAGCTGGCTCAGAGCTCGAGGGCTCAG
Db	91	AGGGCTTTATTCACAGCCACAGGTGCTAGGAGCTGGCTCAGAGCTCGAGGGACTCAG
QY	121	ACAGGCATCTGGATGAGCTGCTCCAGCTGGCTGAGCTGATGAGATGAT
Db	151	ACAGGCATCTGGATGAGCTGCTCCAGCTGGCTGAGCTGATGAT
QY	181	TGCGGACCCCTCAACCTGCAAGTCAGTCAGTCGCTCTGCGTGCACCGAC
Db	211	TGTGACCCCTCAACCCGAACAGCGCCGCTCGTGCACCGAC
QY	241	ATGCCAAGCAGCAGTACAGCCCACTAACACAGAACACAGAGTCCTCA---G
Db	271	ATGCCAAGCAGTCAAGAGTACAGCTCCATCACAGAACATGAGTCAGAG
QY	298	AGAAGAAAGAGAGACATGAAACAGAGTGGAGGAGTCAGGAAACAGAACTA
CC	331	AGAAGAAAGAGAGACATGAAACAGAGTGGAGGAGTCAGGAAACAGAACTA
XX	RESULT	6
XX	AD00405	
XX	ID	AD05405 standard; cDNA; 471 BP.
XX	AC	AAD05405;
XX	DE	10-Aug-2001. (first entry)
XX	DR	Rabbit liver-type IGF-I isoform (L. IGF-I) cDNA.
XX	FH	Rabbit; IGF-I isoform; Insulin-like Growth Factor I; MGF;
XX	KW	mechano-growth factor; neurological disorder; neurodegenerative disorder;
XX	KW	anyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
XX	KW	poliomyelitis; post-polio syndrome; toxin; motoneurone disorder;
XX	KW	nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
XX	KW	sex-linked muscular dystrophy; peripheral neuropathy;
XX	KW	Alzheimer's disease; Parkinson's disease; liver; L. IGF-I; ss.
OS	OS	Oryctolagus cuniculus.
XX	KEY	location/Qualifiers
XX	FT	1..318
XX	CDS	/*tag= a
XX	FT	/product= "Liver-type IGF-I isoform (L. IGF-I)"
XX	FT	/transl_except= (pos:7..9, aa:Gln)
XX	FT	/transl_except= (pos:25..27, aa:Gln)
XX	FT	/note= "These translation exceptions occur while decoding the alternative version of the protein (AAE02456). The CDS comprises exons 3, 4 and 6 and does not include start codon"
XX	FT	/partial
XX	PN	WO200136483-A1.
XX	PD	25-MAY-2001.
XX	PF	15-NOV-2000; 2000WO-3B04354.
XX	PR	15 NOV-1999; 99GB-0026968.
XX	PA	(UNLO) UNIV COLLEGE LONDON.
XX	PI	Goldspink G, Johnson I;
XX	DR	WPI; 2001-3-5620-737.
XX	P-PSDB	AAE02452, AAE02456.
XX	PT	The present invention relates to use of mechano-growth factor (MGF), Factor-I, capable of reducing motoneurone loss, in the manufacture of a medicament for the treatment of neurological disorder -
PT	medicament for the treatment of neurological disorder -	
XX	PS	Disclosure; Page 59-60; 66pp; English.
XX	CC	The present invention relates to use of mechano-growth factor (MGF), Factor-I, capable of reducing motoneurone loss, in the manufacture of a medicament for the treatment of neurological disorder -
CC	CC	an Insulin-like Growth Factor-I (IGF-1) isoform in the manufacture of a medicament for the treatment of neurological disorder. The MGF is capable of reducing motoneurone loss by 20% or greater in response to nerve avulsion, and effects motoneurone rescue, preferably adult motoneurone rescue. The MGF polynucleotide and polypeptide are useful in the manufacture of a medicament for the treatment of a neurological disorder".

Best Local Similarity 87.3%; Pred. No. 5 le-94; Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Db	181 TGTGCCACCCCTAAGCGCCAAGGCAGCCCCGTCGGTGGCCACCGAC	240
Qy		
Db	241 ATGCCAACCCGAGAAGTATCAGCCCCATCTACCAACAAAGAACAGACTACAG	300
Qy		
Db	241 ATGCCAACCCGAGAAGTATCAGCCCCATCTACCAACAAAGAACAGACTACAG	255
Qy	301 AGGAAGAGGAGTACATTGAAAGACACAGTAGGGAGTCCAGGAACAGAACACTACAG	360
Db	256 - - AAGGAGTACATTGAAAGACACAGTAGGGAGTCCAGGAACAGAACACTACAG	311
Qy	361 GATGTA-GAGACCTCAGGAGTGAAGAGACAGCCACGGACCTTGTC	419
Db	312 GATGTA-GAGACCTCAGGAGTGAAGAGACAGCCACGGACCTTGTC	371
Qy	420 TGCAGTACTGTAACCTAACATGCAACGGCAAAATAAGTTGATCACATTCAA	479
Db	372 TGCAGTACTGTAACCTAACATGCAACGGCAAAATAAGTTGATCACATTCAA	431
Qy	480 AGATGGCATTTCCCAATGAATAACACAGTAACT 517	
Db	432 AGATGGCATTTCCCAATGAATAACACAGTAACT 469	

RESULT 8

AAN70436		
ID	AAN70436 standard; cDNA: 818 BP.	
XX		
AC	AAN70436;	
XX		
DT	05-APR-1991 (first entry)	
XX		
DE	Sequence encoding insulin-like growth factor 1A (IGF-1A).	
XX		
KW	Growth promoter; lactation enhancer; cell proliferation; ss.	
XX		
OS	Homo sapiens.	
PN	EP229750-A..	
XX		
PD	22-JUL-1987.	
XX		
PF	06-JAN-1987; 87EP-0870001.	
XX		
PR	20-MOV-1986; 860S-0929671.	
PR	07-JAN-1986; 860S-0816662.	
XX		
PA	(UNIV) UNIV OF WASHINGTON.	
XX		
PI	Krivi GG, Rotwein PS;	
XX		
DR	WPI; 1987-200203/29.	
XX		
PT	New pre-pro-insulin-like growth factor-1 protein - obt'd. by recombinant DNA procedures for use as growth promoters for enhancing lactation, for stimulating cell proliferation etc.	
PT	Example; Fig 5; 59pp; English.	
XX		
CC	A 42 base oligonucleotide corresponding to the DNA sequence encoding amino acids 10 to 23 of mature human IGF-I was synthesized (AAN70437). The radio-labeled 42 mer was then employed to screen for IGF-I containing DNA sequences in a human liver cDNA library. Insulin-like growth factors -1A and -1B cDNAs were isolated from a human cDNA library by using lambdagt 11 (AAN70435, AAN70436). The human IGF-1 gene was isolated and mapped. It encodes at least two proinsulin-like growth factor-1 proteins. An essentially pure proinsulin-like growth factor-1 protein comprising the sequence of amino acids shown in Figure Six is claimed (AAP70277).	
CC	Sequence 818 BP; 232 A; 186 C; 187 G; 213 T; 0 other;	
XX		
SQ	Query Match 66.6%; Score 344.2; DB 8; Length 818;	
XX		

Best Local Similarity 87.3%; Pred. No. 5 le-94; Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

Qy	1 GCACCGAGAGCTCTGGGGCTGAGCTGTGAGCTCTCAGTCAGTCAG 60	
Db	203 GCACGGAGACGCTCTGGGGCTGAGCTGTGAGCTCTCAGTCAGTCAG 262	
Qy	61 AGGGCTTATTCAACAGCCACAGGATGGCTCAGCTGGAGGGCTCTAG 120	
Db	263 AGGGCTTATTCAACAGCCACAGGATGGCTCAGCTGGAGGGCTCTAG 322	
Qy	121 AGGGATCTGATGAGGCTCTGGAGCTGAGTCAGAGGGCTGAGT 180	
Db	323 ACAGGCCTTATTCAACAGCCACAGGATGGCTCAGCTGGAGGGCTGAGT 382	
Qy	181 TGCACACCCCTCAAGGCTGCCAGTCAGCTGCTGTCGCTGCCAGCOCACACGAC 240	
Db	383 TGCACACCCCTCAAGGCTGCCAGTCAGCTGCTGTCGCTGCCAGCOCACACGAC 442	
Qy	241 ATGCCACCCCTGAGCTGAGTCAGCCCCACACTACACAGAAACGAAGT 300	
Db	443 ATGCCACCCCTGAGCTGAGTCAGCCCCACACTACACAGAAACGAAGT 457	

RESULT 9

ABK87583		
ID	ABK87583 standard; cDNA: 7260 BP.	
XX		
AC	ABK87583;	
XX		
DT	14-AUG-2002 (first entry)	
XX		
DE	Human cDNA differentially expressed in granulocytic cells #1154.	
XX		
KW	Human; ss; granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thrombosis; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy; OS	
XX		
OS	Homo sapiens.	
XX		
PN	W0200228999-A2.	
XX		
PD	11-APR-2002.	
XX		
PF	03-OCT-2001; 2001WO-0S30821.	
XX		
PR	03-OCT-2000; 2000US-237189P.	
XX		
PA	(GENE-) GENE LOGIC INC.	
XX		
PI	Beazer-Barclay Y, Weissman SM, Yamaga S, Vockley J;	
XX		

DR WPI; 2002-435328/46.

PT XX detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity -

PT XX

PS Claim 1; SEQ ID NO 1154; 114PB; English.

CC The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA.

CC Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation;

CC (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an agent that modulates the expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful for screening an agent capable of modulating GCA preferably in an inflammation in a tissue; M4 is useful for detecting an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease (e.g. psoriasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosis, cardiac reperfusion injury, renal reperfusion injury, ARDS, adult respiratory distress syndrome, inflammatory bowel disease, Crohn's disease, ulcerative colitis, periodontal disease; also bacterial infection, viral infection, parasitic infection, protozoal infection, fungal infection and M5 is useful for treating one of the above condition. The present sequence represents a gene differentially expressed in granulocytes.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <http://wipo.int/patent/applications/search.html>.

CC CC

XX Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other; 360

Query Match Best Local Similarity 87.3%; Score 344.2; Pred. No. 1.2e-93; Matches 455; Conservative 0; Mismatches 13; Indels 5; Gaps 5;

Qy 1 GAGCCGGAGAGCTCAGGGCGTACGCGGGATGCTTCAGTCAGTGCTGGAGAC 60

Db 311 GAGCCGGAGAGCTCAGGGCGTACGCGGGATGCTTCAGTCAGTGCTGGAGAC 60

Qy 61 AGGGCTTTATTCAACAGCCACAGGTATGGCTCCAGCTCGAGGGCCCTAG 120

Db 371 AGGGCTTTATTCAACAGCCACAGGTATGGCTCCAGCTCGAGGGCCCTAG 430

Qy 121 ACAGGATCGGGAGAGTGGCTCCGGAGCTGTGATCTAAGGGGTGAGATGAT 180

Db 431 ACAGGATCGGGATGAGTGGCTCCGGAGCTGTGATCTAAGGGGTGAGATGAT 490

Qy 181 TCGCACCCCTCAAGCTGCCAAGCTGCCAAGCTGCCAAGGCCACACCGAC 240

Db 491 TCGCACCCCTCAAGCTGCCAAGCTGCCAAGCTGCCAAGGCCACACCGAC 550

Qy 241 ATGCCAGAGCCAGAGTATCAGCCCCATCTACCAACAGAACGAGTCTAGAGA 300

Db 551 ATGCCAGAGCCAGAGTCTAGAGGAGTCAACAGAACGAGTCTAGAGA 565

Qy 301 AGGAAGAGAGAGTACATTGAGAAACAAGTAGAGGGTCAAGAAAGAACACTACAG 360

RESULT 10 ABN97244 ID ABN97244 standard; DNA; 7260 BP.

XX XX

AC ABN97244; XX

DT 13-AUG-2002 (first entry)

XX DE Gene #3742 used to diagnose liver cancer.

XX KW Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic; metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.

XX OS Homo sapiens.

XX PF WO200225103-A2.

XX PR 02-OCT-2000; 2000US-237054P.

XX PD 11-APR-2002.

XX PI Horne D, Alvares C, Peres-Da-Silva S, Vockley JG; DR WPI; 2002-426119/45.

XX DR

PT Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample -

XX

PS Claim 1; SEQ ID NO 3742; 298PP; English.

CC The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ABN97455-ABN97455 in a tissue sample. The method of the invention has hepatotropic and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at <http://wipo.int/patent/applications/search.html>.

XX Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other; 360

Query Match Best Local Similarity 87.3%; Score 344.2; Pred. No. 1.2e-93; Matches 455; Conservative 0; Mismatches 13; Indels 5; Gaps 5;

Matches	455;	Conservative	0;	Mismatches	13;	Indels	53;	Gaps	5;
QY	1	GGACCCSAGAGCCTCGGGGCTGTGAGTCCTCTCAGTGTGAGAC	60						XX
Db	311	GGACCCSAGAGCCTCGGGGCTGTGAGTCCTCTCAGTGTGAGAC	370						XX
QY	61	AGGGCTTTATTCACAAGCCCAAGGGATGGCTCAGAGTCGAGGGCTCAG	120						CC
Db	371	AGGGCTTTATTCACAAGCCCAAGGGATGGCTCAGAGTCGAGGGCTCAG	430						CC
QY	121	ACAGGATCGTGGATAGTGCTTCGGAGCTGTCAGTCAGTGTGAGATST	180						CC
Db	431	ACAGGATCGTGGATAGTGCTTCGGAGCTGTCAGTCAGTGTGAGATST	490						CC
QY	181	TGCGCACCCCTCAAGCTGCCAAGTCAGTCAGTCAGTCAGTCAG	240						CC
Db	491	TGCGCACCCCTCAAGCTGCCAAGTCAGTCAGTCAGTCAGTCAG	550						CC
QY	241	ATGCCAAGCCAGAGTGTAGCTACACACAGAAGCTCAGAGA	360						CC
Db	551	ATGCCAAGCCAGAGCAG	565						CC
QY	301	AGGAAGGAAGTACATTTGAGAACGAACTAGAGGAGTGCGAGGA	621						CC
Db	566	---AGGAAGTAATTTGAGAACGAACTAGAGGAGTGCGAGGA							CC
QY	361	GATGTA-GAAGACCCCTGTGAGGAGGAGGAGGACGGCTTGCTC	419						CC
Db	622	GATGTA-GAAGACCCCTGTGAGGAGGAGGACGGCTTGCTC	681						CC
QY	420	TGCACTAGTACCTG-TAACATGGATAACGGCAAATAATTGATCAC	477						CC
Db	682	TGCACTAGTACCTG-TAACATGGATAACGGCAAATAATTGATCAC	741						CC
QY	478	AAAGAT-GGCATTCCCCAATGAAATACACAGTAAACAT	517						CC
Db	742	AAAGATGGCTTCCCCAATGAAATACACAGTAAACAT	782						CC
RESULT 11									
ABK64812	ID	ABK64812 standard; DNA; 7260 BP.							
XX	XX								
AC	AC	ABK64812;							
DT	DT	18-JUN-2002 (first entry)							
DE	DE	Human benign prostatic hyperplasia gene #707.							
XX	KW	Human; benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.							
OS	OS	Homo sapiens.							
PN	PN	WO200212440-A2.							
PD	PD	14-FEB-2002.							
PF	PF	07-AGS-2001; 2001WO-US24708.							
PR	PR	07-AUG-2000; 2000US-22333P.							
PR	PR	05-JUN-2001; 2001US-0873319.							
PA	PA	(GENE) GENE LOGIC INC.							
PA	PA	(NISB) JAPAN TOBACCO INC.							
PI	PI	Munger WE, Kulkarni P, Getzenberg RH, Waga I, Yamamoto J;							
DR	DR	WPI; 2002-257476/30.							
PT	PT	Identifying drugs for and diagnosing benign prostatic hyperplasia, by detecting expression levels of one or more genes in prostate cells from patient that are differentially regulated compared to normal prostate cells							
RESULT 12									
PS	PS	Disclosure: Page 391-393; 444pp; English.							
XX	XX								
CC	CC	The invention relates to a method of diagnosing (I) the onset or progression of benign prostatic hyperplasia (BPH), or screening (II) for identifying an agent that modulates the onset or progression of BPH, or detecting changes in gene expression in BPH tissue isolated from patients exhibiting different clinical states of prostate hyperplasia as compared to normal prostate tissue. (I) comprises detecting the expression levels of one or more genes in prostate cells from the subject that are differentially regulated compared to normal prostate cells. (II) comprises preparing a first gene expression profile of BPH cells or BPH-like cell population, exposing the cells to the agent, preparing a second gene expression profile of the agent exposed cells, and comparing the first and second gene expression profiles. (I) is useful for diagnosing the onset or progression of BPH. (II) is useful for identifying an agent that modulates the onset or progression of BPH. The methods are useful to present information identifying the expression level in a tissue or cells, by comparing the expression level of genes given in the specification in the tissue or cells to the expression levels of at least one gene in the tissue or cell sample compared to the expression level in BPH. Agents using (II) are useful for treating BPH or prostate cancer. ABK64812 represents human benign prostatic hyperplasia gene sequences of the invention.							
SQ	SQ	Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;							
Query	Match	66.5%; Score 314.2; DB 24; Length 7260;							
Best	Local Similarity	87.3%; Score 314.2; DB 24; Length 7260;							
Matches	455;	Conservative	0;	Mismatches	13;	Indels	53;	Gaps	5;
QY	1	GGACCGAGACGCCTCGGGGGTGAAGTGTGATGCTCTAGTGTGTTGGAGAC	60						XX
Db	311	GGACCGAGACGCCTCGGGGGTGAAGTGTGATGCTCTAGTGTGTTGGAGAC	370						XX
QY	61	AGGGCTTTATTCACAAGCCACAGGGTAGCTCAGACTGGAGCTCAG	120						XX
Db	371	AGGGCTTTATTCACAAGCCACAGGGTAGCTCAGACTGGAGCTCAG	430						XX
QY	121	ACAGGATCGTGGATAGTCGCTTCGGAGCTGTGATCTAGAGGTGAGATG	180						XX
Db	431	ACAGGATCGTGGATAGTCGCTTCGGAGCTGTGATCTAGAGGTGAGATG	490						XX
QY	181	TGGCACCCCTAGCCCTGCCCAGTCAGTCAGTCAGTCAGTCAG	240						XX
Db	491	TGGCACCCCTAGCCCTGCCCAGTCAGTCAGTCAGTCAGTCAG	550						XX
QY	241	ATGCCAAGCCAGAGTATCACCAACAAAGACACAGAACGAGTCAGAGA	300						XX
Db	551	ATGCCAAGCCAGAGCAG	565						XX
QY	301	AGGAAGGAAGTACATTTGAGAACGAACTAGAGGAGTGCGAGGAACAGAACGAG	360						XX
Db	566	---AGGAAGTAATTTGAGAACGAACTAGAGGAGTGCGAGGA							XX
QY	361	GATGTA-GAAGACCCCTGTGAGGAGGAGGAGGACGGCCCGAGGAC	419						XX
Db	622	GATGTA-GAAGACCCCTGTGAGGAGGAGGACGGCCCGAGGAC	681						XX
QY	420	TGCACTAGTACCTG-TAACATGGATAACGGCAAATAATTGATCAC	477						XX
Db	682	TGCACTAGTACCTG-TAACATGGATAACGGCAAATAATTGATCAC	741						XX
QY	478	AAAGAT-GGCATTCCCCAATGAAATACACAGTAAACAT	517						XX
Db	742	AAAGATGGCTTCCCCAATGAAATACACAGTAAACAT	782						XX

AC	ABK35504;	
DT	08-MAY-2002 (first entry)	
XX	Human endometrial cancer related gene, IGF1.	
DE	Human; ds; gene; endometrial cancer; differential expression; DNA microarray; protein microarray.	
KW	Homo sapiens.	
XX	WO200209573-A2.	
XX	07-FEB-2002.	
PD	31-JUL-2001; 2001WO-US24104.	
PF	31-JUL-2000; 2000US-221735P.	
OS	(BGHM) BRIGHAM & WOMENS HOSPITAL INC.	
PA	Mutter GL;	
XX	WPI; 2002-179967/23.	
PI	P-PSDB; AAU84284.	
DR	PT	Diagnosing endometrial cancer comprises determining expression of nucleic acid molecules or expression products that are differentially expressed in normal and malignant endometrium
XX	PS	Claim 1; Page 85-89; 23JPP; English.
XX	The invention relates to diagnosing endometrial cancer in a subject suspected of having endometrial cancer comprising determining the expression of a set of nucleic acid molecules or expression products in an endometrial sample suspected of being cancerous, where the set of nucleic acid molecules comprises at least 2 nucleic acid molecules selected from 50 fully defined sequences as given in the specification. The nucleic acids are used as an array of at least 2 of the 50 nucleic acids bound to a solid substrate. Also included is a solid-phase protein microarray comprising at least 2 antibodies or its antigen binding fragments, that specifically bind at least 2 different polypeptides from the 50 fully defined sequences as given in the specification, fixed to a solid substrate. The methods and arrays are useful for the diagnosis of endometrial cancer, selecting and monitoring treatment regimens and identification of lead compounds useful for the treatment of endometrial cancer. The present sequence is one of 50 genes differentially expressed between cancerous and non-cancerous samples.	
XX	XX	Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;
XX	Query Match	66.6%; Score 344.2; DB 24; Length 7260;
XX	Best Local Similarity	87.3%; Pred. No. 1.2e-93;
XX	Matches 455; Conservative	0; Mismatches 13; Indels 53; Gaps 5;
XX	QY	1 GGACCGAGAGCTCTGGGGCTGAGCTGTGTCAGTCGTGTGAGAC 60
Db	311 GGACCGAGAGCTCTGGGGCTGAGCTGTGAGTCCTCACTGAGAC 370	
QY	61 AGGGGTTTATTCACAGCCACAGGTTATGGTCCACAGTCAGTCAG 120	
Db	371 AGGGGTTTATTCACAGCCACAGGTTATGGTCCACAGTCAGTCAG 430	
QY	121 ACAGGATCGGATGAGTGCTTCCGGAGCTGGATCTAAGAGGGCAGAGGTAT 180	
Db	431 ACAGGATCGGATGAGTGCTTCCGGAGCTGGATCTAAGAGGGCAGAGGTAT 490	
QY	181 TCCGCACCCCTAAGCTGCCAACGAGCTGCTGCTGCTGCTGCCAACCGAC 240	
Db	491 TGGCACCCCTCAAGCTGCCAACGAGCTGGCTGCTGCTGCCAACCGAC 550	
QY	241 ATGCCAAGACCCAGAGTCAAGCCCCATCTACACAAAGACAGGAAGTCAGAGA 300	
XX	RESULT 13	
XX	ABK35561	
XX	ID ABK35561 standard; DNA; 7260 BP.	
XX	AC ABK35561;	
XX	DT 08-MAY-2002 (first entry)	
XX	DE Gene IGF1 differentially expressed in breast cancer tissue.	
XX	KW Human; diagnosis of breast cancer; endometrial cancer; breast tumour; MAI; mitotic activity index; cytostatic; gene; ds.	
XX	OS Homo sapiens.	
XX	PN WO200210436-A2.	
XX	PD 07-FEB-2002.	
XX	XX	PR 27-JUL-2001; 2001WO-US23642.
XX	XX	PR 28-JUL-2000; 2000US-222093P.
XX	XX	PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX	PA (BAK,) BARK J.	
XX	PI Baak J, Mutter GL;	
XX	DR WPI; 2002-180054/23.	
XX	DR P-PSDB; AAU84341.	
XX	PT Diagnosing breast cancer comprises determining expression of nucleic acid molecules or expression products that are differentially expressed in normal and malignant tissue	
XX	PS Claim 1; Page 74-78; 21JPP; English.	
XX	The present invention relates to a method for diagnosing breast cancer in a subject suspected of having endometrial cancer. The method comprises determining the expression of a set of human genes or expression products in an endometrial sample suspected of being cancerous. The human genes of the invention are differentially expressed in breast tumours characterised as high or low MAI (mitotic activity index). These sets of genes can be used to discriminate between high and low MAI breast tumours. The invention also provides DNA and protein microarrays for analysing the expression of the human genes and their protein products. The methods and arrays are useful for the diagnosis and prognosis of endometrial cancer, selecting and monitoring treatment regimens, and identification of compounds useful for the treatment of endometrial cancer. ABK3551-ABK35581 represent the human genes of the invention that are differentially expressed in breast cancer tissue.	
XX	551 ATGCCAAGACCCAG-----	
Db	565	
QY	301 AGGAAAGAGTACATTGAGACAGCTGAGGGAGCAGCAACAGACTACAG 360	
Db	566 --AAGGAAGTACATTGAGAACGAACTAGTGCTGAGGGAGCAGCAACAGACTACAG 621	
QY	361 GATGTA-GAACGACCTCTGAGGAGTGAGAAGGAGCAGGCCAACGGACCTTGCTC 419	
Db	622 GATGTAAGAACCTCTGAGGAGCAGATGACATGCCACGCCAGGATCTTGCTC 681	
QY	420 TGAC-AGTTRACTG-TAACATGATGAAATGCCAACAAATAAGTTGATCACATTC 477	
Db	682 TGCACGAGTACCTGTAACCTGACACCTACCAAAATAAGTTGATCACATTA 741	
QY	478 AAAGAT-GGATTTCGCCCATGAAATACAGAAGTACAT 517	
Db	742 AAAGATGGCCTTCGCCCATGAAATACAGAAGTACAT 782	

SQ	Sequence	7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other;	PI	Goldspink G;
Query Match	66.6%	Score 344.2; DB 24; Length 7260;	XX	WPI: 1997-470877/43.
Best Local Similarity	87.3%	Pred. No. 1.2e 93%;	DR	P-PSDB; AW23302.
Matches	455;	Conservative 0; Mismatches	XX	
Indels	13;		PT	Use of insulin like growth factor I characterised by presence of EC peptide to treat humans or animals, particularly muscle disorders, heart conditions or neuromuscular diseases
Gaps	5;		PT	
Db	311 GGACCGGAGAGCTCTGGGGCTGAATGGCTGTGGTGTCTCAGTCGTTGAGAC	60	XX	
QY	- 61 AGGGGTTTATTAAACAAGCCAGAGGTATGGTCAAGCAGGGTCAAGCAGGGGAGCTAG	120	PS	Disclosure; Fig 4; 33pp; English.
Db	371 AGGGGTTTATTCAACAGCCAGGGPATGGTCAAGCAGGGGAGGGCTCAG	430	XX	
QY	121 ACAGGATCGGGATAGTGTGCTGCTGGAGCTGTTGATCTAAGGGCTGGAGTGAT	180	CC	A use of insulin like growth factor I (IGF-1) has been developed, and is characterised by the presence of the EC peptide, or a functional equivalent, in the treatment or therapy of a human or animal. The IGF-1 polypeptide can be used to treat muscular disorders, e.g. Duchenne or Becker muscular dystrophy, autosomal dystrophies and related progressive skeletal muscle weakness and wasting, muscle atrophy in ageing humans, spinal cord injury induced muscle atrophy and neuromuscular diseases, and cardiac disorders, e.g. diseases where promotion of cardiac muscle protein synthesis is a beneficial treatment, cardiomyopathies and acute heart failure or insult, specifically myocarditis or myocardial infarction. It can also be used to promote bone fracture healing and maintenance of bone in old age. The present sequence encodes human IGF-1 Ea isoform used in the present specification.
Db	431 ACAGGATCGGGATAGTGTGCTGCTGGAGCTGCTGGAGCTGCTGGAGTGAC	490	CC	
QY	181 TCGGACCCCTCAAGCTGGCTGCTGGAGCTGCTGGAGCTGCTGGAGTGAC	240	CC	
Db	491 TCGCACCCCTCAAGCTGGCTGCTGGAGCTGCTGGAGCTGCTGGAGTGAC	550	CC	
QY	241 ATGCCAAGACCCAGAGTATAGCCCACTACACAGAGTCAGAGA	300	CC	
Db	551 ATGCCAAGACCCAG-----	565	CC	
QY	301 AGGAAGGAGTACATTGAGAACAGCAAGTAGGAGGAGCAGAACAGACTACAG	360	XX	
Db	566 ---AGGAAGTACATTGAGAACAGCAAGTAGGAGGACTACAG	621	SQ	Sequence 777 BP; 201 A; 193 C; 204 G; 179 T; 0 other;
QY	361 ATGTA-GAAGACCTCTGAGGAGGAGGAGGAGGACCCAGGACCTTGTC	419	Query Match	66.3%; Score 342.6; DB 18; Length 777;
Db	622 GATGTTAGAACCCCTCTGGGGAGGAGGACTACAG	681	Best Local Similarity	87.1%; Pred. No. 1.5e 93%;
QY	420 TGAC AGTACCTG-TAAATGATGATACGGCCAAAATAAGTTTACATTC	477	Matches	454; Conservative 0; Mismatches
Db	682 TGCACGAGTAACTGTTAACCTACCAAAATAAGTTTACATTC	741	Indels	14; Indels 53; Gaps 5;
QY	478 AAAGAT-GGCATTCGCCAATGAAATACACAAAGTAACAT	517	Db	179 GACCGGAGACGCTCTGGGGCTGAGCTGGATGCTGCTGTTGAGAC
Db	742 AAAGATGGCTTCCCCAACGAAATACACAAAGTAACAT	782	QY	60
RESULT	14		Db	61 AGGGGTTTATTCAACACCCACAGGTATGGTCCACAGCAGTGGAGGGCCTAG
AAT84894			Db	239 AGGGGTTTATTCAACACCCACAGGTATGGTCCACAGCAGTGGAGGT
XX	AAT84894 standard; cDNA; 777 BP.		Db	121 ACAGGATCGTGTGAGTGTGCTTCGGAGCTGTTGATCTAAGGGCTGAT
AC			Db	299 ACAGGATCGTGTGAGTGTGCTTCGGAGCTGTTGATCTAAGGGCTGAT
XX	AAT84894;		QY	181 TCGCACCCCTCAAGCTGGCTGCTGGAGCTGCTGGAGCTGCTGGAGTGAC
DT	14-APR-1998 (first entry)		Db	359 TCGCACCCCTCAAGCTGGCTGCTGGAGCTGCTGGAGCTGCTGGAGTGAC
XX			Db	418
DE	Human insulin like growth factor 1 Ea isoform encoding cDNA.		QY	301 AGGAAGGAGTACATTGAGAACAGCAAGTAGGAGGAGCAGAACAGACTACAG
XX			Db	489
KW	Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;		QY	434 ---AGGAAGTACATTGAGAACAGCAAGTAGGAGGAGCTGCTGGAGTGAC
XX	heart; neuromuscular disease; ss.		Db	419 ATGCCAAGACCCAG-----
OS	Homo sapiens.		QY	361 ATGCCAAGACCCAG-----
XX			Db	419 ATGCCAAGACCCAG-----
FH	Location/Qualifiers		QY	490 GATGTTAGAACCCCTCTGGGGAGCTGCTGGAGCTGCTGGAGTGAC
Key			Db	549
FT	CDS		QY	420 TGAC AGTACCTG-TAAATGATGATACGGCCAAAATAAGTTTACATTC
XX	/ttg= a		Db	477
FT	/product= "IGF-1 Ea isoform"		QY	550 TGCACGAGTAACTGTTAACCTACCAAAATAAGTTTACATTC
XX			Db	609
PN	WO9733997-A1.		QY	478 AAAGAT-GGATTCGCCAATGAAATACACAAAGTAACAT
PD	18-SEP-1997.		Db	517
XX	11-MAR-1997; 97WO-GB00058.		QY	610 AAAGATGGCTTCCCCAACGAAATACACAAAGTAACAT
PR	11-MAR-1996; 96GB-0005124.		Db	650
XX	(UNL0) ROYAL FREE HOSPITAL SCHOOL MED.		AC	AN60490;
XX			RESULT	15
XX			AN60490	
ID	AN60490 standard; mRNA; 622 BP.		XX	
XX			AN60490;	

XX
DT 03-OCT-2002 (updated)
DT 31-JUL-1991 (first entry)
XX
DE Human prepro-somatomedin-C.
XX
KW Sonatomedin-C; ss.
OS Homo sapiens.
XX
Key Location/Qualifiers
CDS 3..360
FT /*tag= a
FT /label= prepro-somatomedin-C
FT mat_peptide 1..254
FT /*tag= b
FT /label= mature somatomedin-C
XX
PN W08600619-A.
XX
PD 30-JAN-1986.
XX
PF 10-JUL-1985;
XX
PR 85WCI-US01325.
XX
13-JUL-1984;
XX
PA (CHIR-) CHIRON CORP.
XX
PI Bell G, Rail LB, Merryweather JP;
XX
DR WPI; 1986-042104/06.
XX
DR P-PSDB; AAP60578.
XX
PS Disclosure; Fig 1; 20pp; English.
XX
The sequence, derived from plasmid phage phigf1, encodes human
prepro-somatomedin-C. The sequence may be used for hormone
production, and is useful for the preparation of DNA probes to
detect the presence of the genes in a natural source. The probes
may be used to detect mutations and/or deletions in humans
suffering from growth deficiencies.
CC See also AAN604B9, AAN60491
CC (Updated on 03-OCT-2002 to add missing OS field.)
XX
Sequence 622 BP; 171 A; 147 C; 161 G; 143 U; 0 other;
XX
Query Match Score 339.4; DB 7; Length 622;
Best Local Similarity 69.6%; Pred. No. 1.3e-92;
Matches 363; Conservative 89; Mismatches 16; Indels 53; Gaps 5;
OY
1 GGACCGGAGAGGTCTCGGGGTGAATCTGTTGAGTCTCTTCAGTGCTGAGAC 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
45 GGACCGGAGAGGTCTCGGGGTGAATCTGTTGAGTCTCTTCAGTGCTGAGAC 104
Db 61 AGGGCTTTATTCAAGAACGCCACAGGGATGGCCACAGCAGGGCAGGGCCTAG 120
OY 181 TGCACACCTCAGCCGCAAGTCAGCTACTCTGCCAGGCCACACCGAC 240
Db 105 AGGGCUCUUAUUCUCAAGAACGCCACAGGGCAGGGCAGGGCUCUAG 164
OY 121 ACAGGATGTTGATGACTGCGCTCGGAGCTGATCAGGAGCTGGAGATGAT 180
Db 165 ACAGGUADUGGAGAUGAGUCUGCUUCGGAGCUGUGAUCAUAGGAGGCGAUGAU 224
OY 225 UGGCCACCCUCAGCCAGGAGAATCTAGCCCCCATCTACCAACAAGAACAGAAGCTCAGAGA 284
Db 241 ATGCCCAAGCCAGAAGATCTAGCCCCCATCTACCAACAAGAACAGAAGCTCAGAGA 300
Db 285 AUGCCCAAGACCCAG----- 299

Qy 301 AGGAAGAAGTACATTGAGAACACAGTAGAGGAGTGCAGGAACAAAGACTACAG 360
Db 300 ---AGGAAGUACAUUUGAGAACGCAAGUAGGGAGCAGGAACAGACAUACAG 355
Qy 361 GATGA-GAACACCTCTAGAGTGAAGAGAGGAGGGCACGGCAGGAGAC 419
Db 356 GAUGUAGGAAGACCUUCUGAGGAGGAGAGUGACAUCCACCGACCGAGAUUUGUC 415
Qy 420 TGCAC-AGTACCTG-TAACATGATACCGGCCAAATAATAGTTGATCACATTC 477
Db 416 UGCAGAGUACCUUACUUTGACACCUCACAAUAGUAGUACAUUA 475
Qy 478 AAAGAT-GGCATTCCCCATGAAATACAACTAACT 517
Db 476 ANAGAUGGGGUUCCCCAUAAGAAUACACAGUAACAU 516

Search completed: June 15, 2003, 16:08:47
Job time : 160.835 secs

GenCore version 5.1.6
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Run on: June 15, 2003, 15:46:38 ; Search time 41.9101 Seconds
(without alignments)
{without alignments}
3783.145 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517
Sequence: 1 ggacggagacgtctcg... tgaatacacaagtaaacat 517

Scoring table: IDENTIV_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*

1: /cgn2_5/ptodata/2/ina/5A.COMB.seq: *
2: /cgn2_5/ptodata/2/ina/5B.COMB.seq: *
3: /cgn2_5/ptodata/2/ina/6A.COMB.seq: *
4: /cgn2_5/ptodata/2/ina/6B.COMB.seq: *
5: /cgn2_5/ptodata/2/ina/PCRS.COMB.seq: *
6: /cgn2_5/ptodata/2/ina/Reactfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

* SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467.4	90.4	553	4	US-09-142-583A-3 Sequence 3, Appli Sequence 5, Appli Sequence 10, Appli Patient No. 5405942
2	467.4	90.4	553	4	US-09-142-583A-5 Sequence 3, Appli Sequence 5, Appli Sequence 10, Appli Patient No. 5405942
3	342.5	66.3	777	4	US-09-142-583A-10 Sequence 3, Appli Sequence 5, Appli Sequence 10, Appli Patient No. 5405942
4	339.4	65.6	622	6	/cgn2_5/ptodata/2/ina/5A.COMB.seq: * Sequence 3, Appli Sequence 5, Appli Sequence 10, Appli Patient No. 5405942
5	286.4	55.4	5707	2	US-08-472-809B-8 Sequence 8, Appli Sequence 7, Appli Patient No. 5405942
6	286.4	55.4	6345	2	US-08-472-809B-7 Sequence 8, Appli Sequence 7, Appli Patient No. 5405942
7	255.2	49.4	357	6	/cgn2_5/ptodata/2/ina/6A.COMB.seq: * Sequence 13, Appli Patient No. 5405942
8	253.5	49.1	357	6	/cgn2_5/ptodata/2/ina/6B.COMB.seq: * Sequence 13, Appli Patient No. 5405942
9	208.4	40.3	210	6	/cgn2_5/ptodata/2/ina/PCRS.COMB.seq: * Sequence 13, Appli Patient No. 5405942
10	208.4	40.3	210	6	/cgn2_5/ptodata/2/ina/Reactfiles1.seq: * Sequence 13, Appli Patient No. 5405942
11	208.4	40.3	2862	4	US-09-255-829-13 Sequence 13, Appli Patient No. 5405942
12	206.8	210	6	5405942-15	SEQUENCE DESCRIPTION: SEQ ID NO: 3:
13	202.8	39.2	240	1	US-08-308-19A-1 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
14	202.8	39.2	240	5	PCT-US91-06452-1 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
15	202.8	39.3	390	3	US-09-267-13 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
16	174.4	33.7	98	1	US-07-933-23A-6 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
17	163.4	31.5	770	1	US-07-933-23A-1 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
18	163.4	31.6	846	1	US-07-933-23A-5 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
19	125.8	24.3	485	1	US-07-989-841-29 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
20	125.8	24.3	485	1	US-07-989-841-13 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
21	125.8	24.3	485	1	US-08-10-663-1 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
22	125.8	24.3	485	1	US-08-159-681-1 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
23	125.8	24.3	485	1	US-08-240-121-13 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
24	125.8	24.3	485	1	US-08-451-241-13 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
25	125.8	24.3	485	1	US-08-110-664-1 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
26	125.8	24.3	485	1	US-08-446-882-1 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
27	125.8	24.3	485	1	US-08-305-187A-1 SEQUENCE DESCRIPTION: SEQ ID NO: 3:

ALIGNMENTS

RESULT 1
US-09-142-583A-3
Sequence 3, Application US/09142583A
Patent No. 6221842

GENERAL INFORMATION:
APPLICANT: GOLOSPINK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADRESSEE: NIXON & VANDERHIE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-OCT-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: NO PCT/GB97/00658
APPLICATION NUMBER: GB 9605124.8
PATENT NUMBER: 5405942
FILING DATE: 11-MAR-1997
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Query Match 90.4%; Score 467.4%; DB 4; Length 553;

Best Local Similarity 95.2%; Pred. No. 1.2e-134;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

QY 1 GGACCGGAGAGCTCTGGGGGCTGAGCTGGATGCTCAGTCGTTGAGAC 60
 Db 31 GAGCCGAGAGCTCTGGGGCTGAGCTGGATGCTCAGTCGTTGAGAC 60
 QY 61 AGGGGCTTATTCAACAGGCCAGGGTATGCTCCAGCAGGGGGCCCTAG 90
 Db 91 AGGGCTTATTCAACAGGCCAGGGTACGGCTCAGCAGTGAGGAGCTAG 150
 QY 121 ACAGGAATGGGAGAGCTGCTCCAGCAGGTGAGCTAAGGGGTGAGAT 180
 Db 151 ACAGGAATGGGAGAGCTGCTCCAGCAGGTGAGCTAAGGGGTGAGAT 180
 QY 181 TGGCACCCCTCAASCTGCCAACGGCCAGGTGCTGGCCAGGCCACCGAC 240
 Db 211 TGTGACCCCTCAASCTGCCAACGGCCAGGTGAGGAGCTGAGATGAC 210
 QY 211 TGTGACCCCTCAASCTGCCAACGGCCAGGTGAGGAGCTGAGATGAC 210
 Db 221 ATGCCAACGCCCTCAAGGCCAGGGTACGGCTCAGTCAGTCAGTCAG 270
 QY 241 ATGCCAACGCCCTCAAGGCCAGGGTACGGCTCAGTCAGTCAGTCAG 297
 Db 271 ATGCCAACACTCAGAGTACGGCTCAGTCAGTCAGTCAGTCAGTCAG 330
 QY 298 AGAGGAAGAGGAGACATTTGAGACAGACAGTAGGGAGTCAGGAACAGACTA 357
 Db 331 AGAGGAAGAGGAGACATTTGAGACAGACAGTAGGGAGTCAGGAACAGACTA 390
 QY 358 CAGGATGA-GAGACCTCTGGAGGAGTAAGAGAACGGACGGACGACCTTG 416
 Db 391 CAGGATGA-GAGACCTCTGGAGGAGTAAGAGAACGGACGGACGACCTTG 450
 QY 417 CTCTGCACAGTACCTGTAACTGGATACCGGGCAAAATAAGTTGACATT 476
 Db 451 CTCTGCACAGTACCTGTAACTGGATACCGGGCAAAATAAGTTGACATT 510
 QY 477 CAAGATGGCTTCCCCATGAAATAACAACTAAT 517
 Db 511 CAAGATGGCTTCCCCATGAAATAACAACTAAT 551

RESULT 2
 US-09-142-583A-5
 ; Sequence 5, Application US/09142583A
 ; Patent No. 6221842
 GENERAL INFORMATION:
 APPLICANT: GOLSPINK, GEOFFREY
 TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P. C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22201

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/142/583A
 FILING DATE: 22-OCT-1998
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/GB97/00658
 FILING DATE: 11-MAR-1997
 ATTORNEY/AGENT INFORMATION:
 APPLICATION NUMBER: GB 9605124.8
 FILING DATE: 11-MAR-1996
 ATTORNEY: SADOFF, B. J.
 NAME: SADOFF, B. J.
 REGISTRATION NUMBER: 36663
 REFERENCE/DOCKET NUMBER: 117-263

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 7038160000
 TELEFAX: 7030164100
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 553 base Pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 341..397
 SEQUENCE DESCRIPTION: SEQ ID NO: 5:
 US-09-142-583A-5

Query Match 90.4%; Score 467.4; DB 4; Length 553;
 Matches 501; Conservative 95.2%; Pred. No. 2e-134;
 Indels 4; Gaps 2;

QY 1 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTCAGTCGTTGAGAC 60
 Db 31 GGACCGGAGACGCTCTGGGGCTGAGCTGGATGCTCAGTCGTTGAGAC 90
 QY 61 AGGGCTTATTCAACAGGCCAGGGTACGGCTCAGTCAGTCAGTCAG 120
 Db 91 AGGGCTTATTCAACAGGCCAGGGTACGGCTCAGTCAGTCAGTCAG 150
 QY 121 ACAGGACGTGATGAGTCGCTCGGGAGCTGATCTAGCTAAGGGCTGAGAT 180
 Db 151 ACAGGACGTGATGAGTCGCTCGGGAGCTGATCTAGCTAAGGGCTGAGAT 210
 QY 181 TGGCACCCCTCAAGGCCAGTCAGCTCGCTCGTCCGAGGCCACACCGAC 240
 Db 211 TGTGACCCCTCAAGGCCAGGGCAAGGCCAGGCCGCTCGTCCGAGGCCACACCGAC 270
 QY 241 ATGCCAACACTCAGAGTACGGCTCAGTCAGTCAGTCAGTCAGTCAG 297
 Db 271 ATGCCAACACTCAGAGTACGGCTCAGTCAGTCAGTCAGTCAGTCAG 330
 QY 298 AGAGGAAGAGGAGACATTTGAGACAGACAGTAGGGAGTCAGGAACAGACTA 357
 Db 331 AGAGGAAGAGGAGACATTTGAGACAGACAGTAGGGAGTCAGGAACAGACTA 390
 QY 358 CAGGATGA-GAGACCTCTGGAGGAGTAAGAGAACGGACGGACGACCTTG 416
 Db 391 CAGGATGA-GAGACCTCTGGAGGAGTAAGAGAACGGACGGACGACCTTG 450
 QY 417 CTCTGCACAGTACCTGTAACTGGATACCGGGCAAAATAAGTTGACATT 476
 Db 451 CTCTGCACAGTACCTGTAACTGGATACCGGGCAAAATAAGTTGACATT 510
 QY 477 CAAGATGGCTTCCCCATGAAATAACAACTAAT 517
 Db 511 CAAGATGGCTTCCCCATGAAATAACAACTAAT 551

RESULT 3
 US-09-142-583A-10
 ; Sequence 10, Application US/09142583A
 ; Patent No. 6221842
 GENERAL INFORMATION:
 APPLICANT: GOLSPINK, GEOFFREY
 TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: NIXON & VANDERHVE P. C.
 STREET: 1100 NORTH GLEBE ROAD
 CITY: ARLINGTON
 STATE: VA
 COUNTRY: USA
 ZIP: 22201
 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/142,583A
 FILING DATE: 23-OCT-1998
 CLASSIFICATION: <unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/GB97/00658
 FILING DATE: 11-MAR-1997
 APPLICATION NUMBER: GB 9605124.8
 FILING DATE: 11-MAR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: SADDE, B. J.
 REGISTRATION NUMBER: 36663
 REFERENCE/DOCKET NUMBER: 117-263
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703/164000
 TELEFAX: 703/164100
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 777 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: both
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 26..493
 SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 ;
 US-09-142-583A-10
 Query Match 66.3%; Score 342.6;; DB 4; Length 777;
 Best Local Similarity 87.1%; Pred. No. 3.8e-96;
 Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;
 Qy 1 GGACGGAGAGCTGCGGGCTGAGCTGGTGGATGCCTTGCTTGTGTTGAGAC 60
 Db 179 GGACGGAGAGCTGCTGGGGCTGAGCTGGTGGATGCCTTGCTTGTGTTGAGAC 238
 Qy 61 AGGGCTTATTACACAGCCACAGGATATGCCAGCAGTCAGCTGGAGGGCCCTAG 120
 Db 239 AGGGCTTATTACACAGCCACAGGATATGCCAGCAGTCAGCTGGAGGGCCCTAG 298
 Qy 121 ACAGCATCTGGTAGCTGCTTCCGGCTGTGATCTAGGAGCTTCAAGAGCTTCAAG 180
 Db 299 ACAGGATCTGGTGGAGCTGCTTCCGGCTGTGATCTAGGAGCTTCAAGAGCTTCAAG 358
 Qy 181 TGGCACCCCTCAAGCTGCCAAGTCAGCTCGCTCTGTCGGCCAGCCACAGAC 240
 Db 359 TGCCGACCCCTCAAGCTGCCAAGTCAGCTCGCTCTGTCGGCCAGCCACAGAC 418
 Qy 241 ATGCCAAGACCCAGAAAGTATGCCAGCCCATCTACCAACAAGAACAGAAGTCTAGAGA 300
 Db 300 ---AAGGAGUACAUUGAAGAACGAGCAGUAGGAGGAGUACAUAGGCUUGGAUGUA 355
 Qy 242 ATGACATCTGGTGGAGCTGCTTCCGGCTGTGATCTAGGAGCTTCAAGAGCTTCAAG 300
 Db 419 ATGCCAAGACCCAG-.....-----.....-----.....-----.....----- 433
 Qy 301 AGGAAGGAGTACATTGAGAACAGAAGTAGGAGGAGTCAGGAACAGAACATACAG 360
 Db 356 GAUGUAGGAGACCCUCUGAGGAGUAGAGUACUGCACGCCAGGACAUUCUUGUC 415
 Qy 420 TGCAC-AGTACCTG-TAACATGGATACCGCCCAAATAAGTTGATCACATTC 477
 Db 416 UGCACGAGUUAACUUGAACACGCCAACACAGAACAGTAACT 517
 Qy 478 AAGAT-GGCATTCCCAAATGAAATACAGAAGTAACT 517
 Db 476 AAGAUGGGCUUCCCCAACUGAAUACACAGUACAU 516
 RESULT 5
 US-08-472-809B-8
 ; Sequence 8, Application US/08472809B
 ; Patent No. 592554
 GENERAL INFORMATION:
 APPLICANT: Schwartz, Robert J.
 APPLICANT: Demayo, Franco J.
 APPLICANT: O'Malley, Bert W.
 TITLE OF INVENTION: Expression vector systems and
 NUMBER OF SEQUENCES: 8
 CORRESPONDENCE ADDRESS:
 ; JAMES P.
 ; I AND II
 ; NUMBER OF SEQUENCES: 16
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/65,673
 ; FILING DATE: 16-JUN-1987
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 630,557
 ; FILING DATE: 19-JUL-1984
 ; SEQ ID NO:2;
 ; LENGTH: 622
 5405942-2
 Query Match 65.5%; Score 339.4;; DB 6; Length 622;
 Best Local Similarity 69.7%; Pred. No. 3.4e-95;
 Matches 363; Conservative 89; Mismatches 16; Indels 53; Gaps 5;
 Qy 1 GGACGGAGAGCTGCGGGCTGAGCTGGTGGATGCCTTGCTTGTGTTGAGAC 60
 Db 45 GGACGGAGAGCTGCTGGGGCTGAGCTGGTGGATGCCTTGCTTGTGTTGAGAC 104
 Qy 61 AGGGCTTATTACACAGCCACAGGATATGCCAGCAGTCAGCTGGAGGGCCCTAG 120
 Db 105 AGGGCUUUAUUCACAGCCACAGGAGUUGGUCCAGGAGUUGGAGGGCCGCUAC 164
 Qy 121 ACGGCAAGCTGCTGGATGAGTCGCTCTGGAGCTGTGATCPAGGGGCTGGAGAT 180
 Db 165 ACAGGUAUCGUGAUGAGUGUCUGUCCGGAGUCAUAGGAGCUUGGUAGAUGUA 224
 Qy 181 TGGCACCCCTCAAGCTGCCAAGTCAGCTCGCTCTGTCGGCCAGCCACAGAC 240
 Db 225 UGCGCACCCUCAGCCAGCCUGCCAGUACGUACGUUGUCCUGCCAGCSCCACAGAC 284
 Qy 241 ATGCCAAGACCCAGAAAGTATGCCAGCCCATCTACCAACAAGAACAGAAGTCTAGAGA 300
 Db 285 AUCCGAGACCCG-.....-----.....-----.....-----.....----- 299
 Qy 301 AGGAAGGAGTACATTGAGAACAGAAGTAGGAGGAGTCAGGAACAGAACATACAG 360
 Db 300 ---AAGGAGUACAUUGAAGAACGAGCAGUAGGAGGAGUACAUAGGCUUGGAUGUA 355
 Qy 361 GATTA-GAAGCCCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGCTTGTC 419
 Db 356 GAUGUAGGAGACCCUCUGAGGAGUAGAGUACUGCACGCCAGGACAUUCUUGUC 415
 Qy 420 TGCAC-AGTACCTG-TAACATGGATACCGCCCAAATAAGTTGATCACATTC 477
 Db 416 UGCACGAGUUAACUUGAACACGCCAACACAGAACAGTAACT 517
 Qy 478 AAGAT-GGCATTCCCAAATGAAATACAGAAGTAACT 517
 Db 476 AAGAUGGGCUUCCCCAACUGAAUACACAGUACAU 516

STREET: 633 West Fifth Street
 CITY: Suite 4700
 STATE: Los Angeles
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C., DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/472,809B
 FILING DATE: June 7, 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/209, 846
 FILING DATE: March 9, 1994
 APPLICATION NUMBER: 07/789, 919
 FILING DATE: November 6, 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 32,327
 REFERENCE/DOCKET NUMBER: 214/212
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEX: (213) 955-0440
 FAX: 67-3510
 FORMATION FOR SEQ ID NO: 8:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5707 bases
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 472-809B-6

Query Match 55.4%; Score 286 4; DB 2; Length 5707;
 Best Local Similarity 85.6%; Pred. No. 1.9e-78;
 Matches 363; Conservative 0; Mismatches 11; Indels 50; Gaps 2;

1 GGACGGGGGAGCCTCTGGGGGCTGAGCTGGTGGAGCTCTCAGTCAGTGGTGTGGAGAC 60
 793 GGACGGGGAGCCTCTGGGGGCTGAGCTGGTGGAGCTCTCAGTCAGTGGTGTGGAGAC 852

61 AGGGGCTTTATTCACAAGGCCAAGGGTAGGGCTGGCTCCAGCAGGGTAGGGTCCAGCAGGGCTCG 120
 853 AGGGGCTTTATTCACAAGGCCAAGGGTAGGGCTGGCTCCAGCAGGGTAGGGTCCAGCAGGGCTCG 912

121 ACAGGCACTGTTGATGAGTGGCTCGCCAGGCTGGATCAAGGGCTGGAGATGT 180
 913 ACAGGCACTGTTGATGAGTGGCTCGCCAGGCTGGAGATGT 972

181 TGGCACCCCTTCAGCTGCAAGCTGGCTCGCCAGGCTGGAGATGT 1032
 973 TGGCACCCCTTCAGCTGCAAGCTGGCTCGCCAGGCTGGAGATGT 1032

241 ATGGCTTGAGACGAGCTTCAGCCCCCATACCAACAGAACAGACTCTAGAGA 300
 1033 ATGCCCAAGACCCAG-----1047

Query Match 55.4%; Score 286 4; DB 2; Length 6345;
 Best Local Similarity 85.6%; Pred. No. 2e-78; Length 6345;
 Matches 363; Conservative 0; Mismatches 11; Indels 50; Gaps 2;

1 GGACGGGGAGCCTCTGGGGGCTGAGCTGGTGTGGAGCTCTCAGTCAGTGGTGTGGAGAC 60
 3702 GGACGGGGAGCCTCTGGGGGCTGAGCTGGTGTGGAGCTCTCAGTCAGTGGTGTGGAGAC 3761

Qy 61 AGGGGCTTTATTCACAAGGCCAAGGGTAGGGCTGGCTCCAGTCAGTGGGGGCCCTCAG 120
 Db 3762 AGGGGCTTTATTCACAAGGCCAAGGGTAGGGCTGGCTCCAGTCAGTGGGGGCCCTCAG 3821

Qy 121 ACAGGCACTGTTGAGTGGCTGGCTCGCCAGGCTGGAGATGT 180
 Db 3822 ACAGGCACTGTTGAGTGGCTGGCTGGCTCGCCAGGCTGGAGATGT 3881

Qy 181 TGGCACCCCTTCAGCTGCAAGCTGGCTCGCCAGGCTGGAGATGT 240
 Db 3882 TGGCACCCCTTCAGCTGCAAGCTGGCTCGCCAGGCTGGAGATGT 3941

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QY          241 ATGCCAAGACCCAGAGTATCAGCCCCATCTACCAACAGAACACCGAAGTCAGAGA 300
Db          3942 ATGCCAAGACCCAG----- 3956
QY          301 AGGAAGGAGTACATTGAGAACACAAGTAGGGGTGAGGAACAGAACTACAG 360
Db          3957 --- AGGAAGTACATTGAGAACAGCAGTGGAGTGAGAAACAGACTACAG 4012
QY          361 GATGTA-GAAGACCTCTGAGGAGTGAAGAAGACGCCACGCCAGACCTTGCTC 419
Db          4013 GATGTAAGGAGACCTCTGAGGAGTGAAGAAGACATGCCACGCCAGATCCCCGGC 4072
QY          420 TGCA 423
Db          4073 TGCA 4076

RESULT 7
5405942-13
; SEQ ID NO:9;
; FILING DATE: 19-JUL-1984
; SEQ ID NO:9;
; LENGTH: 357
; Best Local Similarity 79.2%; Pred. No. 7.1e-59;
; Matches 206; Conservative 50; Mismatches 4; Indels 0; gaps 0;
; Query Match 49.1%; Score 253.6; DB 6; Length 357;
; JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/65,673
; FILING DATE: 16-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 630,557
; FILING DATE: 19-JUL-1984
; SEQ ID NO:13; LENGTH: 357
; SEQ ID NO:13; LENGTH: 357

Query Match      49.4%; Score 255.2; DB 6; Length 357;
Best Local Similarity 90.8%; Pred. No. 2.3e-69;
Matches 257; Conservative 0; Mismatches 3; Indels 0; gaps 0;
; JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
; NUMBER OF SEQUENCES: 15
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/65,673
; FILING DATE: 16-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 630,557
; FILING DATE: 19-JUL-1984
; SEQ ID NO:7; LENGTH: 210
; SEQ ID NO:7; LENGTH: 210

RESULT 9
5405942-7
; SEQ ID NO:9;
; FILING DATE: 19-JUL-1984
; SEQ ID NO:9;
; LENGTH: 210
; Best Local Similarity 79.6%; Pred. No. 4.8e-55;
; Matches 163; Conservative 46; Mismatches 1; Indels 0; gaps 0;
; Query Match 40.3%; Score 208.4; DB 6; Length 210;
; JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/65,673
; FILING DATE: 16-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 630,557
; FILING DATE: 19-JUL-1984
; SEQ ID NO:7; LENGTH: 210
; SEQ ID NO:7; LENGTH: 210

RESULT 8
5405942-9
; Patent No. 5405942
; SEQ ID NO:9;
; LENGTH: 357
; Best Local Similarity 79.2%; Pred. No. 7.1e-59;
; Matches 206; Conservative 50; Mismatches 4; Indels 0; gaps 0;
; Query Match 49.1%; Score 253.6; DB 6; Length 357;
; JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/65,673
; FILING DATE: 16-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 630,557.

RESULT 10
5405942-11
; Patent No. 5405942
; SEQ ID NO:9;
; LENGTH: 357
; Best Local Similarity 79.6%; Pred. No. 4.8e-55;
; Matches 163; Conservative 46; Mismatches 1; Indels 0; gaps 0;
; Query Match 40.3%; Score 208.4; DB 6; Length 210;
; JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/65,673
; FILING DATE: 16-JUN-1987
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 630,557.

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; JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/65,673
; FILING DATE: 16-JUN-1987
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 630-557
; FILING DATE: 19-JUL-1984
; SEQ ID NO:1;
; LENGTH: 210
; 5405942-11

Query Match Similarity 40.3%; Score 208.4; DB 6; Length 210;
Best Local Similarity 99.5%; Pred. No. 4.8e-55;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACCGGAGACGCCTGGGGCTGACSTGCGGATGCTCAGTCAGTGTGTTGAGAC 60
Db 1 GGACCGGAGACGCCTGGGGCTGACSTGCGGATGCTCAGTCAGTGTGTTGAGAC 60
Qy 61 AGGGCTTATTTCACAGCCACAGGTATGGCTCAGACTCGAGGCGCCCTAG 120
Db 61 AGGGCTTATTTCACAGCCACAGGTATGGCTCAGACTCGAGGCGCCCTAG 120
Qy 121 ACAGGATCGGGATGAGCTTCGGAGCTGGAGATGAT 180
Db 121 ACAGGATCGGGATGAGCTTCGGAGCTGGAGATGAT 180
Qy 181 TCGCACCCCTCAAGCTGGCAAGTCAGT 210
Db 181 TCGCACCCCTCAAGCTGGCAAGTCAGT 210

RESULT 11
US-9-255-829-13
Sequence 13, Application US/09255829
Patent No. 6461617
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: STEENE, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REFERENCE/DOCKET NUMBER: 32,893
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

Query Match Similarity 40.3%; Score 208.4; DB 4; Length 2862;
Best Local Similarity 99.5%; Pred. No. 1.5e-54;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 GGACCGGAGACGCCTGGGGCTGACSTGCGGATGCTCAGTCAGTGTGTTGAGAC 2703
Db 2644 GGACCGGAGACGCCTGGGGCTGACSTGCGGATGCTCAGTCAGTGTGTTGAGAC 60
Qy 61 AGGGCTTATTTCACAGCCACAGGTATGGCTCAGACTCGAGGCGCCCTAG 120
Db 2704 AGGGCTTATTTCACAGCCACAGGTATGGCTCAGACTCGAGGCGCCCTAG 2763
Qy 121 ACAGGATCGGGATGAGCTTCGGAGCTGGAGATGAT 180
Db 2764 ACAGGATCGGGATGAGCTTCGGAGCTGGAGATGAT 180
Qy 181 TCGCACCCCTCAAGCTGGCAAGTCAGT 210
Db 2824 TCGCACCCCTCAAGCTGGCAAGTCAGT 2853

RESULT 12
5405942-15
; Patent No. 5405942
; APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRWEATHER,
; JAMES P.
; TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
; I AND II
; NUMBER OF SEQUENCES: 16
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/65,673
; FILING DATE: 16-JUN-1987
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 630-557
; FILING DATE: 19-JUL-1984
; SEQ ID NO:15;
; LENGTH: 210
; 5405942-15

Query Match Similarity 40.0%; Score 206.8; DB 6; Length 210;
Best Local Similarity 77.1%; Pred. No. 1.5e-54;
Matches 162; Conservative 46; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGACCGGAGACGCCTGGGGCTGACSTGCGGATGCTCAGTCAGTGTGTTGAGAC 60
Db 1 GGACCGGAGACGCCTGGGGCTGACSTGCGGATGCTCAGTCAGTGTGTTGAGAC 60
Qy 61 AGGGCTTATTTCACAGCCACAGGTATGGCTCAGACTCGAGGCGCCCTAG 120
Db 61 AGGGCTTATTTCACAGCCACAGGTATGGCTCAGACTCGAGGCGCCCTAG 120
Qy 121 ACAGGATCGGGATGAGCTTCGGAGCTGGAGATGAT 180
Db 121 ACAGGATCGGGATGAGCTTCGGAGCTGGAGATGAT 180
Qy 181 TCGCACCCCTCAAGCTGGCAAGTCAGT 210
Db 181 TCGCACCCCTCAAGCTGGCAAGTCAGT 210

RESULT 13

US-09-308-196A-1

; Sequence 1, Application US/08308196A

; Patent No. 5612198

GENERAL INFORMATION:

APPLICANT: Brierley, Russell A.

APPLICANT: Davis, Geneva R.

APPLICANT: Holtz, Gregory C.

APPLICANT: Gleeson, Martin A.

APPLICANT: Howard, Bradley D.

APPLICANT: Bailey, D. H.

APPLICANT: Gleeson, Martin A.

TITLE OF INVENTION: Production of Insulin-Like Growth

TITLE OF INVENTION: Factor-1 in Methylotrophic Yeast Cells

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDRESS:

ADDRESSEE: Brown, Martin, Haller & McLain

STREET: 1660 Union Street

CITY: San Diego

STATE: California

COUNTRY: USA

ZIP: 92101-2926

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/308,196A

FILING DATE: 09-SEPT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/983,523

FILING DATE: 03-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/578,728

FILING DATE: 04-SEP-1990

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

SEQUENCE CHARACTERISTICS:

REFERENCE/DOCKET NUMBER: 51875

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)238-0999

TELEFAX: (619)238-0062

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 base Pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 14..232

US-08-308-196A-1

RESULT 14

PCU-US91-06452-1

Sequence 1, Application PC/TUS9106452

GENERAL INFORMATION:

APPLICANT: Brierley, Russell A.

APPLICANT: Davis, Geneva R.

APPLICANT: Holtz, Gregory C.

APPLICANT: Gleeson, Martin A.

APPLICANT: Bailey, D. H.

APPLICANT: Gleeson, Martin A.

TITLE OF INVENTION: Production of Insulin-Like Growth

TITLE OF INVENTION: Factor-1 in Methylotrophic Yeast Cells

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fitch, Even, Tabin & Flannery

STREET: 135 South LaSalle Street, Suite 900

CITY: Chicago

STATE: Illinois

COUNTRY: USA

ZIP: 60603

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US91/06452

FILING DATE: 19910409

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/578,728

FILING DATE: 04-SEP-1990

ATTORNEY/AGENT INFORMATION:

NAME: Seidman, Stephanie L.

REGISTRATION NUMBER: 33,779

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619)552-0095

TELEFAX: (619)552-0095

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 240 base Pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

TOPOLOGY: unknown

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 14..232

PCT-US91-06452-1

Query Match

39.2%; Score 202.8; DB 1;

Length 240;

Best Local Similarity 96.7%;

Pred. No. 2.7e-53;

Matches 207; Conservative

0; Mismatches 7;

Indels 0;

Gaps 0;

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60

Db

17 GGACCGAGAGCCTCTGGGGCTAGCTGGTGTCTGAGTCGTTGAGAC

76

QY

61 AGGGCTTATTCACACGCCACAGGTATGCTCCAGCTGAGTCGTTGAGATG

120

Db

77 AGGGCTTATTCACACGCCACAGGTATGCTCCAGCTGAGTCGTTGAGAC

136

QY

121 ACAGGCATCGGAGTAGCTGCTCCAGCTGAGTCGTTGAGATG

180

Db

137 ACAGGCATCGGAGTAGCTGCTCCAGCTGAGTCGTTGAGATG

196

QY

181 TGGCACCCCTCAAGCTGCCAGTCAGCTGCT 214

230

Db

197 TGCGCACCCCTCAAGCTGCCAGTCAGCTGAT 230

RESULT 15

US-09-267-13

Sequence 13, Application US/09029267
 Patent No. 6,170,577
 GENERAL INFORMATION:
 APPLICANT: Crawford, Kenneth
 APPLICANT: Zavor, Isabel
 APPLICANT: Innis, Michael
 TITLE OF INVENTION: Pichia Secretory Leader for Protein
 TITLE OF INVENTION: Expression
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Chiron Corporation
 STREET: 4560 Horton Street
 CITY: Emeryville
 STATE: California
 COUNTRY: United States
 ZIP: 94608
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patient in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/029, 267
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: Chung, Ling Fong
 REGISTRATION NUMBER: 36,482
 REFERENCE/DOCKET NUMBER: 1165.100
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (510) 601-2704
 TELEFAX: (510) 655-3342
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 390 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION:
 /desc = "Synthetic"
 S-09-029-267-13

Query Match 39.2%; Score 202.8; DB 3; Length 390;
 Best Local Similarity 96.7%; Pred. No. 3.e-53;
 Matches 207; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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3	GGGGCTTTTTCACAGGCCACGGTATGGCTCAGGAGCTGAGATCAAGAGCTGGAGTGAT	180
4	ACAGGGATCGGATGATGCTGGCTCAGGAGCTGAGCTGAT 214	240
5	TGGCACCCCTAACGGTGCAGCTGGAGCTGAGATCTAAGAGGCTCGAGATGAT	279

61 AGGGGTTTATTTCACAAACGCCAGGGATGGTCCAGCTGGAGGGGCTCAG 219
 62 AGGGGTTTATTTCACAGGCCACGGTATGGCTCAGGAGCTGAGATCAAGAGCTGGAGTGAT 273
 63 AGGGGTTTATTTCACAGGCCACGGTATGGCTCAGGAGCTGAGATCAAGAGCTGGAGTGAT 339

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Job time : 43.9101 secs

Om nucleic - nucleic search, using sw model

Run on: June 15, 2003, 17:22:19 ; Search time 93.6428 seconds
 (without alignments)
 7.94.713 Million cell updates/sec

Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	517	100.0	517	Sequence 1, Appli
2	467.4	90.4	523	Sequence 5, Appli
3	73.0	471	10	US-09-852-261-1 Sequence 13, Appli
4	344.2	66.6	7260	Sequence 4, Appli
5	344.2	66.6	7260	Sequence 24, Appli
6	65.5	7260	10	US-09-919-497-24 Sequence 37, Appli
7	325.2	62.9	539	Sequence 10, Appli
8	318.2	61.5	651	Sequence 1, Appli
9	50.7	318	9	US-10-161-088-1 Sequence 9, Appli
10	247.8	47.9	487	Sequence 11, Appli
11	228	44.1	462	Sequence 1, Appli
12	204.6	39.6	4532	Sequence 1, Appli
13	203.6	39.4	210	US-09-930-377B-2 Sequence 3, Appli
14	202.8	39.2	390	US-10-179-046-13 Sequence 13, Appli
15	140.2	27.1	286	Sequence 3, Appli
16	140.2	27.1	213	US-10-076-815-9 Sequence 9, Appli
17	140.2	27.1	9	US-10-077-381-9 Sequence 9, Appli
18	123.8	23.9	621	US-10-280-824-40 Sequence 40, Appli
19	123.8	23.9	621	US-09-921-398-40 Sequence 40, Appli

ALIGNMENTS

RESULT 1

US-09-852-261-1

; Sequence 1, Application US/09852261
 ; Patent No. US0020083477A1
 ; GENERAL INFORMATION
 ; APPLICANT: GOLDSPIKIN, GEOFFREY
 ; INVENTOR: TERENGHI, GIORGIO
 ; TITLE OR INVENTION: REPAIR OF NERVE DAMAGE
 ; FILE REFERENCE: 117-351
 ; CURRENT APPLICATION NUMBER: US/09-852-261
 ; CURRENT FILING DATE: 2001-05-10
 ; PRIOR APPLICATION NUMBER: GB 001278.9
 ; PRIOR FILING DATE: 2000-05-10
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 1
 ; LENGTH: 517
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens

US-09-852-261-1

Query Match 100.0%; Score 517; DB 10; Length 517;
 Best Local Similarity 100.0%; Pred. No. 1.2e-159; Indels 0;
 Matches 517; Conservative 0; Mismatches 0; Gaps 0;

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 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 1 GGACGGGAGACCTCTGGGGCTGACCTGGATGCCCTCAGTCGTGTGAGAC 60

Do : 1 AGGCGTTTATTCACAAAGCCACAGGTTAGGCCTCACAGTGGAGGGCTCAG 120
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 61 AGGGCTTTATTCACAAAGCCACAGGTTAGGCCTCACAGTGGAGGGCTCAG 120
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 61 AGGGCTTTATTCACAAAGCCACAGGTTAGGCCTCACAGTGGAGGGCTCAG 120
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 121 AGGGCATCTGATGAGTGCTGCTGGAGCTGATCAAGGGCTGAGATGAT 180
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 121 AGGGCATCTGATGAGTGCTGCTGGAGCTGATCAAGGGCTGAGATGAT 180
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 181 TGGCACCCCTAACGCCAGCTGCAAGTCAGTCGCTGCTGGAGGGCTCAG 240
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 181 TGGCACCCCTAACGCCAGCTGCAAGTCAGTCGCTGCTGGAGGGCTCAG 240
 ||||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 241 ATGCCAGAACGAGGATCAGCCCCCATCTACCAACAGAACAGAGCTCAGAGA 300


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Sequence 4 Application US/10136639
Publication No. US20030072161A1
GENERAL INFORMATION:
APPLICANT: Lebowitz, Jonathan
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TARGETING PROTEINS ACROSS THE BLOOD
TITLE OF INVENTION: BARRIER
FILE REFERENCE: SYM-008
CURRENT APPLICATION NUMBER: US/10/136,639
CURRENT FILING DATE: 2003-09-06
PRIORITY APPLICATION NUMBER: US 60/329,650
PRIORITY FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 7260
TYPE: DNA
ORGANISM: Homo sapiens
US-10-136-639-4

Query Match 66.6%; Score 344.2; DB 9; Length 7260;
Best Local Similarity 87.3%; Pred. No. 2.8e-102; Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

QY 1 GGACCCGAGAGCTCTGGGGGTGAGCTGGGATGCTCTAGTGGAGAC 60
311 GGACCCGAGAGCTCTGGGGGTGAGCTGGGATGCTCTAGTGGAGAC 370
Db 61 AGGGCTTTTCAACAGGCCACAGGTTATGCTCAGGGATGCTCCAG 120
371 AGGGCTTTTCAACAGGCCACAGGTTATGCTCAGGGATGCTCCAG 430
Db 121 ACAGGCATCGGGATGAGTGGCATCCGGAGCTGATTAAGAGGTGGAGAT 180
431 ACAGGCATCGGGATGAGTGGCATCCGGAGCTGATTAAGAGGTGGAGAT 490
Db 181 TGGCACCCCTAACGGCTGCCAACGTCAGCTGGCTCTGCGCTGCGGCCAGCAGCACCGAC 240
491 TGGCACCCCTAACGGCTGCCAACGTCAGCTGGCTCTGCGCTGCGGCCAGCAGCACCGAC 550
Db 241 ATGCCAGACCCAGAAATTATCACAGAACAGGAGTCAGCCCATCTACCAACAAGAACAGGAAGCTCAGAGA 300
551 ATGCCAGACCCAGAAATTATCACAGAACAGGAGTCAGCCCATCTACCAACAAGAACAGGAAGCTCAGAGA 565
Db 301 AGGAAAGAGTACATTGAGAACACAGTGGAGGTTGAGATGAT 360
566 ---AAGAGTACATTGAGAACACAGTGGAGGTTGAGATGAT 621
Db 361 GAIGTA-GAGACCTTGAGGAGTGGAGAACAGGACAGGCCACCGCACCGAC 419
622 GATGTAGAGACCTCTTGAGGAGTGGAGATGACCGACAGGAGTGGCTC 681
Db 420 TGCACTGTTACCTG-TAACATGGATAACCGCCAAATAAGTTGATAACATTA 747
682 TGACAGAGTACCGTTAACATGGATAACCGCCAAATAAGTTGATAACATTA 741
Db 478 AAAGAT-GGCATTCGCCCAATGAATAACAGTAACAT 517
742 AAAGATGGCGTTCCCCAATGAATAACAGTAACAT 782

RESULT 5
US-09-919-497-24
; Sequence 24, Application US/09919497
; Patent No. US2002010662A1
; GENERAL INFORMATION:
; APPLICANT: Mutter, George L.
; TITLE OF INVENTION: PROGNOSTIC CLASSIFICATION OF ENDOMETRIAL CANCER
; FILE REFERENCE: B0B017725
; CURRENT APPLICATION NUMBER: US/09/919,497
; CURRENT FILING DATE: 2001-07-31
; PRIORITY APPLICATION NUMBER: US 60/221,735
; PRIORITY FILING DATE: 2000-07-31
; NUMBER OF SEQ ID NOS: 100

; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 24
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025

Query Match 66.6%; Score 344.2; DB 10; Length 7260;
Best Local Similarity 87.3%; Pred. No. 2.8e-102; Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

QY 1 GGACCCGAGAGCTCTGGGGGTGAGCTGGGATGCTCTAGTGGAGAC 60
311 GGACCCGAGAGCTCTGGGGGTGAGCTGGGATGCTCTAGTGGAGAC 370
Db 61 AGGGCTTTTCAACAGGCCACAGGTTATGCTCAGGGATGCTCCAG 120
371 AGGGCTTTTCAACAGGCCACAGGTTATGCTCAGGGATGCTCCAG 430
Db 121 ACAGGCATCGGGATGAGTGGCATCCGGAGCTGATTAAGAGGTGGAGAT 180
431 ACAGGCATCGGGATGAGTGGCATCCGGAGCTGATTAAGAGGTGGAGAT 490
Db 181 TGGCACCCCTAACGGCTGCCAACGTCAGCTGGCTCTGCGCTGCGGCCAGCAGCACCGAC 240
491 TGGCACCCCTAACGGCTGCCAACGTCAGCTGGCTCTGCGCTGCGGCCAGCAGCACCGAC 550
Db 241 ATGCCAGACCCAGAAATTATCACAGAACAGGAGTCAGCCCATCTACCAACAAGAACAGGAAGCTCAGAGA 300
551 ATGCCAGACCCAGAAATTATCACAGAACAGGAGTCAGCCCATCTACCAACAAGAACAGGAAGCTCAGAGA 565
Db 301 AGGAAAGAGTACATTGAGAACACAGTGGAGGTTGAGATGAT 360
566 ---AAGAGTACATTGAGAACACAGTGGAGGTTGAGATGAT 621
Db 361 GAIGTA-GAGACCTTGAGGAGTGGAGAACAGGACAGGCCACCGCACCGAC 419
622 GATGTAGAGACCTCTTGAGGAGTGGAGATGACCGACAGGAGTGGCTC 681
Db 420 TGCACTGTTACCTG-TAACATGGATAACCGCCAAATAAGTTGATAACATTA 747
682 TGACAGAGTACCGTTAACATGGATAACCGCCAAATAAGTTGATAACATTA 741
Db 478 AAAGAT-GGCATTCGCCCAATGAATAACAGTAACAT 517
742 AAAGATGGCGTTCCCCAATGAATAACAGTAACAT 782

RESULT 6
US-09-880-107-3739
; Sequence 3739, Application US/09880107
; Patent No. US200102981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-05-14
; PRIORITY APPLICATION NUMBER: US 60/211,379
; PRIORITY FILING DATE: 2000-06-14
; PRIORITY APPLICATION NUMBER: US 60/237,054
; PRIORITY FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3739
; LENGTH: 7260
; TYPE: DNA
; ORGANISM: Homo sapiens
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 X57025

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US-09-880-107-3739

Query Match 66.6%; Score 344.2; DB 10; Length 7260;
Best Local Similarity 87.3%; Pred. No. 2.8e-102;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

QY 1 GGACCGGAGAGCTGGGGCTGAGCTGGATGCTCAGTGTGAGGAGCTGGAGAC 60
311 GGACCGGAGAGCTGGGGCTGAGCTGGATGCTCAGTGTGAGGAGCTGGAGAC 60
Db 61 AGGGCTTTATTCACAAAGCCACAGGGTAGCTGGATGCTCAGTGTGAGGAGCTGGAGAC 120
371 AGGGCTTTATTCACAAAGCCACAGGGTAGCTGGATGCTCAGTGTGAGGAGCTGGAGAC 120
Db 121 ACAGGCATTTGTTGAGTGGTTGCTCCAGCTGAGCTGGAGGAGCTGGAGAC 180
QY 181 TCGGACCCCTCAAGGCCCTCAACTCAGTCAGTCAGTGTGAGGAGCTGGAGAC 240
Db 181 TGTGICGICGCAAGCCCTACAAAGTCAGCTGTTCCAGGAGCTGGAGAC 240
QY 241 ATGCCAAGACCCAGAAATCACGCCCATCTACCAAGAACAGACAGTCTCA -- G 297
121 ACAGGCATTTGTTGAGTGGCTGGCTCCAGGAGCTGGAGGAGCTGGAGAC 180
Db 431 ACAGGCATTTGTTGAGTGGCTGGCTCCAGGAGCTGGAGGAGCTGGAGAC 430
QY 551 ATGCCAAGACCCAGAAATCACGCCCATCTACCAAGAACAGACAGTCTCA 490
Db 551 ATGCCAAGACCCAGAAATCACGCCCATCTACCAAGAACAGACAGTCTCA 490
QY 566 ---AAGGAGTACATTGAGAACGAGCTGGAGGAGCTGGAGAACAGACTACAG 565
301 AGGAAGAGAGAGATGAGAACACAAGTAGAGGAGGAGGAGGAGGAGGAGGAG 360
QY 361 GAGCTA-GAGAACCTTGTAGGAGTGGAGCTGGAGGAGGAGGAGGAGGAGGAG 419
622 GAATGAGGAGAACCTTGTAGGAGTGGAGCTGGAGGAGGAGGAGGAGGAGGAG 681
Db 420 TGCG-AGTACCTG-TAACATGGATACTGGCCAAAATAAGTTGTACACATTTC 477
Db 682 TGCAGGAGTACCTGTAACATGGACACCTTACCAAAATAAGTTGTACACATTTC 741
QY 478 AAGAT-GCCATTCCCCATGAAATCACAGTAACAT 517
Db 742 AAAGATGGGGTTCCCCATGAAATCACAGTAACAT 782

RESULT 7

US-09-852-261-3

; Sequence 3: Application US/09852261
; Patent No. US20020084477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPINK, GEOFFREY
; APPLICANT: TERENGHI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: SE 0101934-8
; PRIOR FILING DATE: 2001-06-01
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 651
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE: CDS
; NAME/KEY: CDS
; LOCATION: (73)..(471)
; US-10-161-088-1

Query Match 62.9%; Score 325.2; DB 10; Length 539;
Best Local Similarity 81.2%; Pred. No. 1.4e-95;
Matches 429; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

SEQ ID NO 3
LENGTH: 539
; TYPE: DNA
; ORGANISM: Rattus sp.
; US-09-852-261-3

Query Match 62.9%; Score 325.2; DB 10; Length 539;
Best Local Similarity 81.2%; Pred. No. 1.4e-95;
Matches 429; Conservative 0; Mismatches 88; Indels 11; Gaps 4;

QY 1 GGACCGGAGAGCTGGGGCTGAGCTGGATGCTCAGTGTGAGGAGCTGGAGAC 60
1 GGACCGAGAGCTGGGGCTGAGCTGGATGCTCAGTGTGAGGAGCTGGAGAC 60
Db 61 AGGGCTTTATTCACAAAGCCACAGGGTAGCTGGATGCTCAGTGTGAGGAGCTGGAGAC 60
QY 199 AGGGCTTTATTCACAAAGCCACAGGGTAGCTGGATGCTCAGTGTGAGGAGCTGGAGAC 60
Db 139 GGACCGAGAGCTGGGGCTGAGCTGGATGCTCAGTGTGAGGAGCTGGAGAC 198
QY 61 AGGGCTTTATTCACAAAGCCACAGGGTAGCTGGATGCTCAGTGTGAGGAGCTGGAGAC 120
Db 259 ACAGGCATTTGTTGAGTGGCTGGCTCCAGGAGCTGGATGCTGTTGAGGAGCTGGAGAC 318
QY 181 TCGCACCCCTCAAGCCAGTCAGCTGGCTGGCCAGGCCACACCGAC 240

319 TGTGCCCACTGAAAGCCTAACAAACGGCCCTATCGGCCAGGCCACTGAC 378

GENERAL INFORMATION:
APPLICANT: GOLSPINK, GEOFFREY

APPENDIX: TEBENGI, GIORGIO
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE

FILE REFERENCE: 117_351
CURRENT APPLICATION NUMBER: US/09/852, 261

CURRENT FILING DATE: 2001-05-10
PRIORITY NUMBER: GB 0011278.9

PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 11

LENGTH: 487
TYPE: DNA

ORGANISM: Rattus sp.
US-09-852-261-11

Query Match 47.9% Score 247.8; DB 10; Length 487;
Best Local Similarity 74.5%; Pred. No. 3; 5e-7; 0; Mismatches 77; Indels 57; Gaps 4;
Matches 391; Conservative 0; Mismatches 77;

QY 1 GGACCGGAGCCTCTGGGGCTGAGCTGGTGGAGCTCAGTCAGTCAGTCAG 60

Db 1 GGACCGGAGCCTCTGGGGCTGAGCTGGTGGAGCTCAGTCAGTCAGTCAG 60

QY 61 AGGGCTTTTACTCAACAGCCACAGCTATGGCTCAGGCACAGCAG 120

Db 61 AGGGCTTTTACTCAACAGCCACAGCTATGGCTCAGGCACAGCAG 120

QY 121 ACAGCACATGGTAGAGCTGGCTCGAGCTGGTCTAGAGCTGAGAT 180

Db 121 ACAGCACATGGTAGAGCTGGCTCGAGCTGGTCTAGAGCTGAGAT 180

QY 181 TGCCACCCCTCAAGCCGCCAGTCACTCTGCTGCGGCCAGGCCACACCGAC 240

Db 181 TGCCACCCCTCAAGCCGCCAGTCACTCTGCTGCGGCCAGGCCACACCGAC 240

QY 182 AGGGCTTTATTCAACAGCCACAGGGATGGCTCCAGCTGGAGGGGCCCTCAG 120

Db 182 AGGGCTTTATTCAACAGCCACAGGGATGGCTCCAGCTGGAGGGGCCCTCAG 120

QY 241 ATGCCAAGACCCAGAGTA 260

Db 241 ATGCCAAGACCCAGAGTA 260

RESULT 9
US-09-852-261-9

Sequence 9, Application US/09852261
Patent No. US20020083477A1

GENERAL INFORMATION:
APPLICANT: GOLDSPINK, GEOFFREY

APPENDIX: TERENCI, GIORGIO
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE

FILE REFERENCE: 117_351
CURRENT APPLICATION NUMBER: US/09/852, 261

CURRENT FILING DATE: 2001-05-10
PRIORITY NUMBER: GB 0011278.9

PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 14

SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 11

LENGTH: 487
TYPE: DNA

ORGANISM: Rattus sp.
US-09-852-261-11

Query Match 47.9% Score 247.8; DB 10; Length 487;
Best Local Similarity 74.5%; Pred. No. 3; 5e-7; 0; Mismatches 77; Indels 57; Gaps 4;
Matches 391; Conservative 0; Mismatches 77;

QY 1 GGACCGGAGCCTCTGGGGCTGAGCTGGTGGAGCTCAGTCAGTCAGTCAG 60

Db 1 GGACCGGAGCCTCTGGGGCTGAGCTGGTGGAGCTCAGTCAGTCAGTCAG 60

QY 61 AGGGCTTTTACTCAACAGCCACAGCTATGGCTCAGGCACAGCAG 120

Db 61 AGGGCTTTTACTCAACAGCCACAGCTATGGCTCAGGCACAGCAG 120

QY 121 ACAGCACATGGTAGAGCTGGCTCGAGCTGGTCTAGAGCTGAGAT 180

Db 121 ACAGCACATGGTAGAGCTGGCTCGAGCTGGTCTAGAGCTGAGAT 180

QY 181 TGCCACCCCTCAAGCCGCCAGTCACTCTGCTGCGGCCAGGCCACACCGAC 240

Db 181 TGCCACCCCTCAAGCCGCCAGTCACTCTGCTGCGGCCAGGCCACACCGAC 240

QY 182 AGGGCTTTATTCAACAGCCACAGGGATGGCTCCAGCTGGAGGGGCCCTCAG 120

Db 182 AGGGCTTTATTCAACAGCCACAGGGATGGCTCCAGCTGGAGGGGCCCTCAG 120

QY 241 ATGCCAAGACCCAGAGTA 260

Db 241 ATGCCAAGACCCAGAGTA 260

RESULT 9
US-09-852-261-9

Sequence 9, Application US/09852261
Patent No. US20020083477A1

GENERAL INFORMATION:
APPLICANT: GOLDSPINK, GEOFFREY

APPENDIX: TERENCI, GIORGIO
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE

FILE REFERENCE: 117_351
CURRENT APPLICATION NUMBER: US/09/852, 261

CURRENT FILING DATE: 2001-05-10
PRIORITY NUMBER: FR 01 11736

PRIOR FILING DATE: 2001-09-11
PRIORITY NUMBER: US 60/318, 665

Query Match 47.9% Score 247.8; DB 10; Length 487;
Best Local Similarity 74.5%; Pred. No. 3; 5e-7; 0; Mismatches 77; Indels 57; Gaps 4;
Matches 391; Conservative 0; Mismatches 77;

QY 1 GGACCGGAGCCTCTGGGGCTGAGCTGGTGGAGCTCAGTCAGTCAGTCAG 60

Db 1 GGACCGGAGCCTCTGGGGCTGAGCTGGTGGAGCTCAGTCAGTCAGTCAG 60

QY 61 AGGGCTTTTACTCAACAGCCACAGCTATGGCTCAGGCACAGCAG 120

Db 61 AGGGCTTTTACTCAACAGCCACAGCTATGGCTCAGGCACAGCAG 120

QY 121 ACAGCACATGGTAGAGCTGGCTCGAGCTGGTCTAGAGCTGAGAT 180

Db 53 ACAGCACATGGTAGAGCTGGCTCGAGCTGGTCTAGAGCTGAGAT 180

QY 181 TGCCACCCCTCAAGCCGCCAGTCACTCTGCTGCGGCCAGGCCACACCGAC 240

Db 30 TGCCACCCCTCAAGCCGCCAGTCACTCTGCTGCGGCCAGGCCACACCGAC 240

QY 182 AGGGCTTTATTCAACAGCCACAGGGATGGCTCCAGCTGGAGGGGCCCTCAG 120

Db 5 AGGGCTTTATTCAACAGCCACAGGGATGGCTCCAGCTGGAGGGGCCCTCAG 120

QY 241 ATGCCAAGACCCAGAGTA 260

Db 0 ATGCCAAGACCCAGAGTA 260

RESULT 11
US-09-852-261-11

Sequence 1, Application US/1033814
Publication No. US2003010073A1

GENERAL INFORMATION:

APPLICANT: Merial

APPENDIX: ANDREONI, Christine Michele VACCINE ADJUVANT, IN PARTICULAR AGAINST FELINE

FILE REFERENCE: 454413-3165.1

CURRENT APPLICATION NUMBER: US/10/238, 114

PRIOR APPLICATION NUMBER: FR 01 11736

PRIOR FILING DATE: 2001-09-11

PRIORITY NUMBER: US 60/318, 665

Query Match 47.9% Score 247.8; DB 10; Length 487;
Best Local Similarity 74.5%; Pred. No. 3; 5e-7; 0; Mismatches 77; Indels 57; Gaps 4;
Matches 391; Conservative 0; Mismatches 77;

QY 1 GGACCGGAGCCTCTGGGGCTGAGCTGGTGGAGCTCAGTCAGTCAGTCAG 60

Db 1 GGACCGGAGCCTCTGGGGCTGAGCTGGTGGAGCTCAGTCAGTCAGTCAG 60

QY 61 AGGGCTTTTACTCAACAGCCACAGCTATGGCTCAGGCACAGCAG 120

Db 30 AGGGCTTTTACTCAACAGCCACAGCTATGGCTCAGGCACAGCAG 120

QY 121 ACAGCACATGGTAGAGCTGGCTCGAGCTGGTCTAGAGCTGAGAT 180

Db 5 ACAGCACATGGTAGAGCTGGCTCGAGCTGGTCTAGAGCTGAGAT 180

RESULT 11
US-09-852-261-11

Sequence 1, Application US/1033814
Publication No. US2003010073A1

PRIOR FILING DATE: 2001-09-12
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 1
 LENGTH: 462
 TYPE: DNA
 ORGANISM: Felis catus
 ; US-10-238-114-1

Query Match

Best Local Similarity 44.1%; Score 228; DB 9; Length 462;

Matches 240; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Db 145 GGACAGAGAGCTGCGGGCTGAGCTGGTGTGAGTCAGTGTTGAGAC 204

Qy 61 AGGGCTTTATTCAACAGCACAGCCACASGGTATGGCTCAGCAGCTGGAGGCCCTAG 120

Db 205 AGGGCTTTATTCAACAGCACAGCCACASGGTATGGCTCAGCAGCTGGAGGCCCTAG 264

Qy 121 ACAGCATGGTGGAGCTGTCTGTCGGAGCTGAGCTTAAGGAGGTGAGATAT 180

Db 265 ACAGCATGGTGGAGCTGTCTGTCGGAGCTGAGCTTAAGGAGGTGAGATAT 324

Qy 181 TGCACCCCTCAAGCTGCCAGTCAGCTCGCTGRCCTGCCCCAGGCCAACCGAC 240

Db 325 TGTGACCCCTCAAGCTGCCAGTCAGCTGCCAGTCAGCTGCTCACGCCACATGAC 384

Qy 241 ATGCCAAGGCCAGAGTA 260

Db 385 ATGCCAAGGCCAGAGTA 404

RESULT 12

US-09-930-377B-1

Sequence 1, Application US/09930377B

Patent No. US2002014296A1

GENERAL INFORMATION:

APPLICANT: Wheeler, Matthew B.

APPLICANT: Donovan, Sharon M.

APPLICANT: Bleck, Gregory T.

APPLICANT: Monaco-Seigel, Marcia

TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk

FILE REFERENCE: 66-00

CURRENT APPLICATION NUMBER: US/09/930,377B

PRIORITY FILING DATE: 2001-08-15

PRIORITY FILING DATE: 2000-08-15

NUMBER OF SEQ ID NOS: 2

SEQ ID NO 2

LENGTH: 210

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:IGF-I

US-09-930-377B-2

Query Match

Best Local Similarity 98.1%; Score 203; DB 10; Length 210;

Matches 206; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 GGACGGAGAGCTGCGGGCTGAGCTGGTGTGAGTCAGTGTTGAGAC 60

Db 1 GGACGGAGAGCTGCGGGCTGAGCTGGTGTGAGTCAGTGTTGAGAC 60

Qy 61 AGGGCTTTATTCAACAGCACAGCCACASGGTATGGCTCAGCAGCTGGAGGCCCTAG 120

Db 61 AGGGCTTTATTCAACAGCACAGCCACASGGTATGGCTCAGCAGCTGGAGGCCCTAG 120

Qy 2046 GGACGGAGAGCTGCGGGCTGAGCTGGTGTGAGTCAGTGTTGAGAC 2105

Db 61 AGGGCTTTATTCAACAGCACAGCCACASGGTATGGCTCAGCAGCTGGAGGCCCTAG 2105

Qy 2106 AGGGCTTTATTCAACAGCACAGCCACASGGTATGGCTCAGCAGCTGGAGGCCCTAG 2165

Qy 121 ACAGCATGGTGGAGCTGCTGGAGCTGGAGCTGGAGATGT 180

RESULT 13

US-09-930-377B-2

Sequence 2, Application US/09930377B

Patent No. US2002014296A1

GENERAL INFORMATION:

APPLICANT: Wheeler, Matthew B.

APPLICANT: Donovan, Sharon M.

APPLICANT: Bleck, Gregory T.

APPLICANT: Monaco-Seigel, Marcia

TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk

FILE REFERENCE: 66-00

CURRENT APPLICATION NUMBER: US/09/930,377B

PRIORITY FILING DATE: 2001-08-15

PRIORITY FILING DATE: 2000-08-15

NUMBER OF SEQ ID NOS: 2

SEQ ID NO 2

LENGTH: 210

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Description of Artificial Sequence:IGF-I

US-09-930-377B-2

Query Match

Best Local Similarity 98.1%; Score 203; DB 10; Length 210;

Matches 206; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 1 GGACGGAGAGCTGCGGGCTGAGCTGGTGTGAGTCAGTGTTGAGAC 60

Db 1 GGACGGAGAGCTGCGGGCTGAGCTGGTGTGAGTCAGTGTTGAGAC 60

Qy 61 AGGGCTTTATTCAACAGCACAGCCACASGGTATGGCTCAGCAGCTGGAGGCCCTAG 120

Db 61 AGGGCTTTATTCAACAGCACAGCCACASGGTATGGCTCAGCAGCTGGAGGCCCTAG 120

Qy 121 ACAGCATGGTGGAGCTGCTGGAGCTGGAGCTGGAGATGT 210

Db 121 ACAGCATGGTGGAGCTGCTGGAGCTGGAGCTGAAGTCAGCAGCTGGAGATGT 210

Qy 181 TGCACCCCTCAAGCTGCCAGTCAGCT 210

Db 181 TGCACCCCTCAAGCTGCCAGTCAGCT 210

RESULT 14

US-10-179-046-13

Sequence 13, Application US/10179046

Publication No. US2003013154A1

GENERAL INFORMATION:

APPLICANT: Crawford, Kenneth

APPLICANT: Zaror, Isabel

TITLE OF INVENTION: Pichia Secretary Leader for Protein Expression

NUMBER OF SEQUENCES: 40

CORRESPONDENCE ADDRESS:

ADDRESSEE: Chiron Corporation

STREET: 4560 Horton Street

CITY: Emeryville

STATE: California

COUNTY: United States

ZIP: 94608

COMPUTER READABLE FORM:

	Matches	220;	Conservative	0;	Mismatches	30;	Indels	0;	Gaps
QY	16	TGCGGGCTGAGCNGTGGATGCTTCAGTCGNGTGGAGCAGGGCTTTATTTC	75						
Db	18	TGCAGGGCTGAGCTGGATGCTTCAGTCGNGTGGAGCAGGGCTTTATTTC	77						
QY	76	ACAAAGCCACAGGTATGCCAGCAGTGCGAGGAGGCGCCCTCACAGACGGCATCGTATGAT	135						
Db	78	CTCTGCAAGTGCTGCTGGAGCTGCTGATGCTGAGCTGGAGGAGGCGCCCTCACAGACGGCATCGTATGAT	137						
QY	136	GAGTGCTGCTTCGGAGCTGATGCTAAGGAGGAGMGTATIGGCACCCCTCAAG	195						
Db	138	GAGTGCTGCTTCGGAGCTGATGCTGAGGAGACTGGAGTGTACTGTGCCCACTGAAG	197						
QY	196	CCTGCCAAGTAGCTGCTGCTGTCGTCGCCAGGCCACCCGACATGCCAASICCCAG	255						
Db	198	CCTACAAAAGCAGGCCGCTATCGTGCCTGCCAACATGCCAGACTGACATGCCAAGACTCAG	257						
QY	256	AAGTATCAGC	265						
Db	258	GCATGCAAGC	267						
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Job time : 95.6428 secs									
US-10-179-046-13									
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Best Local Similarity 96.7%; Pred. No. 2e-56; Matches 207; Conservative 0; Mismatches 7; Indels 0; Gaps 0;									
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Db	150	GGACGGGAGACGCTGGGGGGAGGTGGTGGATGCGTCAAGGCTGAGTCAGTGTGAGGAGAC	219						
Qy	61	AGGGCTTTATTCAGAAGGCCACAGGTGCTTCAGCAGTGGCTCGAGCTGGAGGCGCTCAG	120						
Db	220	AGGGCTTTATTCAGAAGGCCACAGGTGCTTCAGCAGTGGCTCGAGCTGGAGGCGCTCAG	279						
Qy	121	ACAGGCACTGGATGAGTGGCTCGGAGGTGTGATCTAAGGAGGCTGGAGATGAT	180						
Db	280	ACAGGCACTGGATGAGTGGCTCGGAGGTGTGATCTAAGGAGGCTCGAGATGAT	339						
Qy	181	TGGCACCCCTGAGGCCAGCTGAGTCAGTCGGT	214						
Db	340	TGGCACCCCTGAGGCCAGCTGAGTCAGTCGGT	373						
RESULT 15									
US-10-161-088-3									
Sequence 3; Application US/10161088									
Publication No. US2003007761A1									
GENERAL INFORMATION:									
APPLICANT: Parlow, Vendela									
APPLICANT: Rosegren, Linda									
TITLE OF INVENTION: NEW METHODS									
FILE REFERENCE: 13425-11101									
CURRENT APPLICATION NUMBER: US/10/161.088									
CURRENT FILING DATE: 2002-05-31									
PRIOR APPLICATION NUMBER: SE 0101934-8									
PRIOR FILING DATE: 2001-06-01									
NUMBER OF SEQ ID NOS: 3									
SOFTWARE: FastSEQ for Windows Version 4.0									
SEQ ID NO 3									
LENGTH: 286									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-10-161-088-3									

GenCore version 5.1.6
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OM nucleic - nucleic search, using a sw model

Run on: June 15, 2003, 15:41:03 ; Search time 1099.81 seconds
{without alignments} 7613.181 Million cell updates/sec

Title: US-09-852-261-1
Perfect score: 517
Sequence: 1 ggacccggagacgtctggg.....tgaatacacaaatcaaact 517

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: em_estba:
2: em_esthum:
3: em_estin:
4: em_lesmu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_htc:
9: gb_est1:
10: gb_est2:
11: gb_hic:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: gb_gss:
18: em_gss_hum:
19: em_gss_inv:
20: em_gss_phn:
21: em_gss_vrt:
22: em_gss_fun:
23: em_gss_mam:
24: em_gss_mus:
25: em_gss_other:
26: em_gss_pro:
27: em_gss_rod:

RESULT 1
LOCUS A1503976/c 558 bp mRNA linear EST 11-MAR-1999
DEFINITION vna3d08_x1 Stratagene mouse diaphragm (1937303) MUS musculus cDNA
CLONE IMAGE-1001007 3' similar to gb:x04482 Mouse mRNA sequence.
PREPROINSULIN-LIKE GROWTH FACTOR IB (MOUSE);, mRNA sequence.
ACCESSION A1503976.1
VERSION GI:4401827
KEYWORDS EST.
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS 1 (bases 1 to 558)
Marr,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Person
Underwood,K., Steptoe,M., Theising,B., Allen,M., Powers,V., Person
B., Swaller,T., Gibbons,M., Pepe,D., Harvey,N., Schurk,R., Ritter
,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterson,R., and Wilson,R.
Waterson,N.C.I. Mouse EST Project 1999
Unpublished (1999)
Contact: Marla.M.Watson-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 285 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LINL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	Comment
C 1	331.6	64.1	558	A1503976 vna3d08_x1	Unpublished (1999)
C 2	330.6	63.9	14	BW984670 UI-CP-EC1	Contact: Marla.M.Watson-NCI Mouse EST Project 1999
C 3	329.8	63.8	623	AW16128 un37e0.0.x	Washington University School of Medicine
C 4	326.6	63.2	575	A1248089	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
C 5	316.6	61.2	549	A116253 EST2.5.088	Tel: 314 285 1800
C 6	315.8	61.1	558	A1265629 uj04b07.x	Fax: 314 286 1810

MG:565223
 This clone was previously sequenced on the 5' end only, this new
 data is from the 3' end
 High quality sequence stop: 440.

FEATURES

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 /db_xref="taxon:10090"
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 /clone_libr="Stratagene mouse diaphragm (#937303)"
 /tissue_type="diaphragm"
 /dev_stage="adult"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
 prepared from diaphragm muscle. Primer: Oligo dT. Average
 insert size: 1.5 kb. Uni-ZAP XR vector; -5' adaptor
 sequence: 5' GAATTCGACAG 3' ~3' adaptor sequence: 5'
 CTOGAGCTTTTTTTTTTTT 3'"
 103 a 133 c 149 g 173 t

BASE COUNT

ORIGIN

Query Match 64.1%; Score 331.6; DB 9; Length 558;
 Best Local Similarity 82.0%; Pred. No. 1.4e-87;
 Matches 433; Conservative 0; Mismatches 84; Indels 11; Gaps 4;

QY

1 GGACGGAGCGCTGCAGGGCTGAGCTGATGTCCTCAGTCGTGTTGGAGAC 60
 530 GGACAGAGCCCTTGCGGGCTGAGCTGCTTCAGTGTGTTGGAGAC 471

Db

61 AGGGCTTATTCAACAGGCCAACAGGATGCTCAGCAGTCGAGGGCCAG 120
 470 AGGGCTTATTCAACAGGCCAACAGGATGCTCAGCAGTCGAGGGCCAG 471

QY

121 ACASCATGTTACTCAACAGGCCAACAGGATGCTCAGCAGTCGAGGGCCAG 180
 121 ACASCATGTTACTCAACAGGCCAACAGGATGCTCAGCAGTCGAGGGCCAG 180

Db

410 ACAGGATTTGGATGAGTGTGTTGGAGCTGAGGAGATGGAGATGAC 351
 181 TGCACACCCCTCAAGCCGCCAGCTGAGCTGCTGAGGAGCTGAGGAGAC 240
 350 TGTGCCCACTGAAAGCTACAAAGCAGCCGCTATCGTGTGCCAGCCACATGAC 291

QY

241 ATGCCAACACCCAGAACATCACCCCCATCTAACACAAGAACAGAACGCTA -- 297
 290 ATGCCAACACCCAGAACATCACCCCCATCTAACACAAGAACAGAACGCTAAG 231

Db

298 AGANGGAAGGAGTACATTGAGAACAGTAGAGGGAGTCAGAACAGAACAGACTA 357
 230 AGANGGAAGGAGTACATTGAGAACAGTAGAGGGAGTCAGAACAGAACAGACTA 171

QY

358 CAGATGTA-GAGACCTCTGAGGGAGAGGAGGCCACGGGACCTTG 416
 170 CAGATGTTAGGAGGCCACGCCAGGAGAAATGCCACATCACGGCATGGCTCTG 111

Db

417 CTCTCACACTTACCTGTAAACATGGATAACGGCCA---AAAATAAGTTGATC 470
 110 CTGCTTGAGAACCTGCAAACATGAAACCTACCAATAACATTAAGTCCATA 51

QY

471 ACATTCAGAGATGGCATTCGCCAATGAAATACAGATAACAT 517

Db

50 ACATACAAAGATGGCATTCGCCAATGAAATACAGATAACAT 3

RESULT

2

BM934670/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE	AUTHORS	JOURNAL	MEDLINE	COMMENT
Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 673)	Bonaldo, M.F., Lennon, G. and Soares, M.B.	Normalization and subtraction: two approaches to facilitate gene discovery. Genome Res. 6 (9), 791-806 (1996)		
				Tissue Procurement: Dr. M. J. Welsh, University of Iowa cDNA Library preparation: Dr. M. Bentz Soares, University of Iowa DNA Sequencing by: Dr. M. Bentz Soares, University of Iowa -Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com). Seq. primer: M13 FORWARD
POLY=A:Yes	Location/Qualifiers			
	source			
	1. . 673			
	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	/clone="UI-CF-EC1-abj-k-24-0-UI"			
	/clone_libr="UI-CF-EC1"			
	/tissue_type="Lung"			
	/dev_stage="Adult and Fetal"			
	/lab_host="DH10B (Life Technologies) (T1 phage resistant)"			
	/note="Organ: Lung; Vector: pT13-Pac (Pharmacia) with a modified Polylinker; Site_1: Ecor I; Site_2: Not I; UICF-EC1 is a normalized cDNA library containing the following tissue(s): Normal lung from adult and from fetal day 64, day 87, week 19 and week 42. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo(dT) primer containing a Not I site. Double stranded cDNA was ligated to an Ecor I adaptor, digested with Not I, and cloned directionally into pT13-Pac vector. The oligonucleotide used to prime the synthesis of first strand cDNA contains a library tag sequence that is located between the Not I site and the poly(A) tail. The sequence tag for this library is TAG LIB=UICF-EC1. TAG LIB=UICF-EC1			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
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	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
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	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
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	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
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	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
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	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
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	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
	Matches 453; Conservative 0; Mismatches 14; Indels 54; Gaps 6;			
	Query Match 63.9%; Score 330.6; DB 14; Length 673;			
	Best Local Similarity 86.9%; Pred. No. 2.9e-87;			
</				

		Custom primers for sequencing: 5' end primer CTTCCTCTTAAACTGCG and 3' end primer CGACCTGCAGCTGRCACA.
OY	241 ATGCCCAAGACCCAGAGTATCAGCCCCATCTACCAACAGAACCGAAGTCTCGAGAG 	300
Db	253 ATGCCCAAGACCCAG -----	239
OY	301 AGGAAGAGGAGACTACATTGGAGAACACAAGTAGGGAGCTGAGAAAGAACAGACTACG 	360
Db	238 ---AAGGAAGAGACTACATTGGAGAACACAAGTAGGGAGCTGAGAAAGAACAGACTACG -----	183
OY	361 GATGTA-GAAGACCTCTGAGGGAGTGAGGGAGCAGGCCACCGAGACCTTGCTC 	419
Db	182 GATGTA-GAAGACCTCTGAGGGAGTGAGGGAGCAGGCCACCGAGACCTTGCTC 	123
OY	420 TGGAC-AGTACCTG-TAAAGATGGATACCGGCAAANATAAGTTGATCACATTC 	477
Db	122 TGCACGAGTTCCTGTAACTTGACACTACAAAAAATAAGTTGATCACATTA 	63
OY	478 AAGAT-GGCATTCGCCAAATGAAATACACAGTAACAT 	517.
Db	62 AAGATGGCCTTCCCCAATGAAATACACAGTAACAT 	22
RESULT 3		
AW146128/c		
LOCUS	AW146128	623 bp mRNA linear EST 10-oct-2000
DEFINITION	um7e10.x1 Sugano mouse embryo newa Mus musculus cDNA clone	
IMAGE:	2247498	3' similar to gb:XU4482 Mouse mRNA for proprotein convertase 1B (MOUSE); mRNA sequence.
ACCESSION	AW146128	
VERSION	AW146128.1	GT:6167864
KEYWORDS	EST.	
ORGANISM	Mus musculus	
BELARUS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
REFERENCE	1 (bases 1 to 623)	
AUTHORS	Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steetoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, I., Jackson, Y., Cardenas, M., McCann, R., Waterston, R., and Wilson, R.	
TITLE	The WashU-NCI Mouse EST Project 1999	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Marra/M/WashU-NCI Mouse EST Project 1999	
FEATURES	source	
	1. -623	
	Location/Qualifiers	
	1. mouseest@watson.wustl.edu	
	This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	
	MGU-100958	
	Seq. Primer: custom primer used	
	High quality sequence stop: 499.	
RESULT 4		
AW1248089/c		
LOCUS	AW1248089	575 bp mRNA linear EST 01-DEC-1998
DEFINITION	gh69f05.x1 Soares_fetal_liver_spleen.INSLS_SI Homo sapiens DNA clone IMAGE:18x953	
GROWTH FACTOR	IA PRECURSOR (HUMAN); mRNA sequence.	
ACCESSION	AW1248089	
VERSION	AW1248089.1	GT:3843486
KEYWORDS	EST.	
ORGANISM	Homo sapiens	
BELARUS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 (bases 1 to 575)	
AUTHORS	NCI-NCAP http://www.ncbi.nlm.nih.gov/ncap.	
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
JOURNAL	Unpublished (1997)	
COMMENT	Contact: Robert Strausberg, Ph.D.	
FEATURES	source	
	Email: cgaps-f@mail.nih.gov	
	This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	
	Insert Length: 918 Std Error: 0.00	
	Seq. Primer: -400P from Gibco	
	High quality sequence stop: 380.	
	Location/Qualifiers	

source

1. .575 .

/organism="Homo sapiens"

/db_xref="Taxon:9606"

/clone="IMAGE:849953"

/sex="male"

/dev_stage="20 week-post conception fetus"

/lab_host="DH110B (ampicillin resistant)"

/note="Organ: Liver and Spleen; Vector: pT7³D (Pharmacia)

with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;

This is a subtracted version of the original Soares fetal

liver spleen INFLS library. 1st strand cDNA was primed

with a Pac I - oligo(dT) primer [5'-AATGGAAGATTAATTAACATTCGTTTTTTTTT 3'],

double-stranded cDNA was ligated to Eco RI adaptors

(Pharmacia), digested with Pac I and cloned into the Pac I

and Eco RI sites of the modified pT7³D vector. Library

went through one round of normalization. Library

constructed by Bento Soares and M. Fatima Bonaldo."

1 others

BASE COUNT

135 a 152 c 131 g 156 t

1 others

ORIGIN

Query Match

63.2%; Score 326.6; DB 9; Length 575;

Best Local Similarity

86.6%; Pred. No. 4; e=86;

Matches 438; Conservative 0; Mismatches 15; Indels 53; Gaps 5;

QY

16 TCGGGGCTGAGCTGGAGAGCTCAGTGGTGTGAGACAGGGCTTATTTC

75

Db

551 TGCGGGCGAGCTGGTGTAGTCAGTCAGTGTGAGACAGGGCTTATTTC

492

QY

76 AACAGGCCAACAGGATATGCCTCAGACTGGAGGGCCCTAGACGGCACGCGAT

135

Db

491 AACAGGCCAACAGGATATGCCTCAGACTGGAGGGCCCTAGACGGCACGCGAT

432

QY

136 GAGTGTGCTCCGAGCTGTAAGGAGCTGGAGATGTATTGGCAACCTCAAG

195

Db

431 GAGTGTGCTCCGAGCTGTAAGGAGCTGGAGATGTATTGGCAACCTCAAG

372

QY

196 CCTSCCAASCTAGCTGCTGCTGCGTCCACCGCCACCGACATGCCAGACCG

255

Db

371 OCTGCGCAAGCTAGCTGCCTCTGCGGICGCCACACCATGCCACGAGCCAG

312

QY

256 AAGTTCACGCCCATCTACACAAGACACAGTCAGAAGAAAGAAAGTACA

315

Db

311 -----AAGAAAGTACA 301

QY

316 TTGAGAACACANGTAGAGGCTGAGAACAGACTCAGGAGTGAAAGACCC

374

Db

300 TTGAGAACACANGTAGAGGCTGAGAACAGACTCAGGAGTGAAAGACCC

241

QY

375 TTGAGAACACANGTAGAGGCTGAGAACAGACTCAGGAGTGAAAGACCC

433

Db

240 TCTGAGGAGCTGAGAGTCATGCCACCGCAGATCCPTTGCTCGACAGTAC

181

QY

434 -TAAACATGATACCGGCAAAATAATAGTTGATCACATTCAAGAT-GGCATTC

491

Db

180 TAACTTGGACACTACCAAATAATAGTTGATCACATTAAAGATGGGCTTC

121

QY

492 CCCATGATACCAAGTAAACAT 517

Db

120 CCCATGATACCAAGTAAACAT 95

RESULT 5

All6253/c

LOCUS A169253

DEFINITION 549 bp mRNA linear EST 08-JAN-1999

ACCESSION ESR215088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone

VERSION A169253

KEYWORDS A169253.1 GL:4134375

SOURCE EST.

ORGANISM Rattus sp.

REFERENCE

AUTHORS Lee, N.H., Giodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Keilwitz, A.R. and Adams, M.D.

TITLE Rat Genome Project: Generation of a Rat EST Catalog & Rat Gene Index

COMMENT Unpublished (1998) On Oct 6, 1998 this sequence version replaced gi:3705561.

Other_Eenis: TC50779 Contact: Lee, NH

The Institute for Genomic Research

9712, Medical Center Drive, Rockville, MD 20850, USA

Tel: (301)-838-3529

Fax: (301)-838-0508

Email: nilee@igrid.org

Seq primer: M13-21.

FEATURES

source

1. .549 Location/Qualifiers

/organism="Rattus sp."

/db_xref="taxon:10118"

/clone="RKB1033"

/clone_lib="Normalized rat kidney, Bento Soares"

/note="Organelle: kidney; Vector: pT7/p3Pac; Site_1: EcoRI;

BASE COUNT

112 a 140 c 133 g 164 t

ORIGIN

Query Match

61.2%; Score 316.6; DB 9; Length 549;

Best Local Similarity

80.8%; Pred. No. 4; e=83;

Matches 421; Conservative 0; Mismatches 89; Indels 11; Gaps 4;

QY

8 AGACGTCTGGGGTGGAGTGTCTCAGTCAGTCGTTGTTGAGACAGGGCT

67

Db

549 AGACCTCTGGGGCTGACTGGGGCTCTTCATTCATTCGTTGTTGAGACAGGGCT

490

QY

68 TTATTCACAGCCACGGTAGCTGCTCAGAGTCGTCGGGGGCCAGACGGCA

127

Db

489 TTACTCAAGCCACAGGTAGTCGCTCAGTCAGTCGCTCAGTCAGACGGGCA

430

QY

128 TCGTGGTAGAGTGTCTCGGGAGGTGTGAGCTAGAGGGCTGGAGATGATGCGC

187

Db

429 TTGTGGTAGAGTGTCTCGGGAGGTGTGAGCTGGAGGCTGGAGAATGACTGTGTC

370

QY

188 CCCTCAAGCCCTGCGCAAGTCAGCTGCTCTGCGGCCAGCGACAGGCCA

247

Db

369 CGCTGAGGCCTACAAAGTCAGTCAGTCGTTCCATCGGGCCAGCGGCCACATGCGCA

310

QY

248 AGACCGAAGTATGCCACCATTCACCAACAGACAGACAGCTCA--GAGAGGA

304

Db

309 AGCTCAGAGTCGCCACCCCTATCGACACAGAACAGGCTGCAAGAGGAGGA

250

QY

305 AGGAAGTACATTGAGAACAGAGTAGAGGAGTCAGGAACAGAACATCAGGATG

364

Db

249 AGGAAGTACATTGAGAACAGAGTAGAGGAGTCAGGAACAGAACATCAGAATG

190

QY

365 TA-GAGACCTCTGGAGTAGAGGACAGGCCACGGACCTTGCTGCTGCA

423

Db

189 TAGGAGGACCCAGAACAGAACATGCGACGCCAGCAAGTATCCTTGCTGCTG

130

QY

424 CAGTACCTGAAACATGGATACGGCC-----AAATAATGTTACATTC

477

Db

129 AGCAACCTGCAACACATGGAACACCTGGCAATTCATAATGAGTCATACATT

70

QY

478 AAAGAT-GGCATTCGCCACATGAACTACAGTAACAT 517

Db

69 AGGATGGSCATTCCATGAACTACAGTAACAT 29

RESULT 6

A1265629/c

LOCUS A1265629

DEFINITION 558 bp mRNA linear EST 18-NOV-1998

DEFINITION [uj04507.x1 Sugano mouse liver mla Mus musculus cDNA clone IMAGE:189050113'](#), similar to [gb:X041882 Mouse mRNA for preproctolin-like growth factor IB \(MOUSE\)](#); mRNA sequence.

ACCESSION A1265629
VERSION A1265629.1
KEYWORDS EST
SOURCE mouse
ORGANISM Mus musculus

REFERENCE 1 (bases 1 to 558)
AUTHORS Marmur,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubroque,T., Ceisel,S., Kucaba,T., Lacy,M., Lee,M., Martin,J., Morris,M., Scheibenbogen,B., Stepko,M., Tan,F., Underwood,K., Moore,B., Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE The WashU-HMMI Mouse EST Project
COMMENT Unpublished (1996)
Contact: Maria M/Mouse EST Project
WashU-HMMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (infoimage.lnl.gov) for further information.

SEQ PRIMER: custom primer used
High quality sequence stop: 495.

FEATURES source
1. .558
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL"
/clone="IMAGE:1890901"
/db_xref="txon:10090"
/clone_id="Sugano mouse liver mla"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: liver; Vector: pME18S-FL3; Site-1: DraIII (CACCTGCG); Site-2: DraIII (CACCAGTG); 1st strand cDNA was primed with an oligo(dt) primer (ATGGGGCCTTTTCCTTTCCTT); double-stranded cDNA was ligated to a DraIII adaptor (TCTGGGCTAATGG), digested and cloned into distinct DraIII sites of the pME18S-FL3 vector (5' site CACCTGCG, 3' site CACCAGTG). XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Sciences). Custom primers for sequencing: 5' end primer CTTCCTGCTTAAAGCTGG and 3' end primer CGACCTGCAGCTGGACCA."
BASE COUNT ORIGIN
106 a 135 c 156 g 161 t

Query Match 61.1%; Score 315.8; DB 9; Length 558;
Best Local Similarity 80.8%; Freq. No. 7e-83;
Matches 408; Conservative 0; Mismatches 87; Indels 10; Gaps 3;
QY 1
Db 506
QY 61
Db 446
QY 121
Db 386
QY 181

DEFINITION [AA542914/c](#)
LOCUS AA542914
DEFINITION ni98210.s1 NCI-CGAP-Pr21 Homo_sapiens cDNA clone IMAGE:984882 3', similar to [gb:X57025_mRNA INSULIN-LIKE GROWTH FACTOR 1A PRECURSOR \(HUMAN\)](#); mRNA sequence.

ACCESSION AA542914
VERSION AA542914.1
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 498)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/cicgap>
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsposr@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnl.gov/borp/Imager/Image.html
Insert Length: 603 Std Error: 0.00
Seq Primer: -4:0m13 fwd. Et from Amersham
High quality sequence stop: 412.

FEATURES source
1. .498
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="txon:9600"
/clone_id="NCI-CGAP_Pr21"
/sex="male"
/tissue_type="normal prostate"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pRT73D-Pac (Pharmacia)
with a modified Polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligorotamer primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library is not normalized. Library was constructed by Bent Soares and M. Fatima Bonaldo."

DEFINITION [326](#) [TGTCGCCCACTGAGCTACAAGAGGCCGCTATCCGTGCCAGCSCACACTGAC](#) 267
Db 326
QY 241 [ATGCCCAAGACCCAGAGATACTGCCCATCTACACAGAACAGAACGAGCTCA-G](#) 297
Db 265 [ATGCCCAAGACTCAGAGTCCCGCTCCATGAGAACACAGTAGGAGTGCAGGAAACAGACTGA](#) 207
QY 298 [AGAGGAGAGAGAGTACATTGAGAACAGTAGTAGGGAGTGCAGGAAACAGACTA](#) 357
Db 206 [AGAGGAGAGAGAGTACATTGAGAACACAGTAGGAGTGCAGGAAACAGACTGA](#) 147
QY 358 [CAGGATGAGAGACAGTACATTGAGAACACAGTAGGAGTGCAGGAAACAGACTA](#) 416
Db 146 [CAGATGAGAGAGTACATTGAGAACACAGTAGGAGTGCAGGAAACAGACTGA](#) 87
QY 417 [CTCTGACAGTACCTGTAACATTGAGAACACAGTAGGAGTGCAGGAAACAGACTA](#) 470
Db 86 [CTCTGAGCAACCTGCAACATCGAACACACTAACATACATATAGTCATA](#) 27
QY 471 [ACATTCAAGATGGCATTCCTCC](#) 495
Db 26 [ACATTCAAAGATGGCATTCCCC](#) 2

RESULT ?
ACCESSION AA542914
DEFINITION AA542914
LOCUS AA542914
DEFINITION ni98210.s1 NCI-CGAP-Pr21 Homo_sapiens cDNA clone IMAGE:984882 3', similar to [gb:X57025_mRNA INSULIN-LIKE GROWTH FACTOR 1A PRECURSOR \(HUMAN\)](#); mRNA sequence.

ACCESSION AA542914
VERSION AA542914.1
KEYWORDS EST
SOURCE human
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 498)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/cicgap>
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgsposr@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www.bio.lnl.gov/borp/Imager/Image.html
Insert Length: 603 Std Error: 0.00
Seq Primer: -4:0m13 fwd. Et from Amersham
High quality sequence stop: 412.

FEATURES source
1. .498
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="txon:9600"
/clone_id="NCI-CGAP_Pr21"
/sex="male"
/tissue_type="normal prostate"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pRT73D-Pac (Pharmacia)
with a modified Polylinker; 1st strand cDNA was prepared from normal prostate bulk tissue, and was then primed with a Not I - oligorotamer primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pRT3 vector. Library is not normalized. Library was constructed by Bent Soares and M. Fatima Bonaldo."

BASE COUNT
105 a 135 c 123 g 135 t

ORIGIN

Query Match 60.9%; Score 314.8; DB 9; Length 498;
 Best Local Similarity 86.2%; Pred. No. 1.3e-82; Mismatches 17;
 Matches 450; Conservative 0; Mismatches 17; Indels 55; Gaps 7;

FEATURES	source
/organism="Mus musculus"	
/strain="C57BL"	
/db_xref="taxon:10090"	
/clone="IMAGE:1498803"	
/dev_stage="embryo, 14 dpc"	
/lab_host="DH10B;"	
/note="Vector: PM18S-FL3; Site_1: DraIII (CACTGTTG); Site_2: DraIII (CACCTATG); 1st strand cDNA was primed with an oligo(dt) primer (ATGGCCCTTTCCTTTCCTT); double stranded cDNA was ligated to a DraIII (TGTGGCCATCGG) digested and cloned into distinct DraIII sites of the PME18S-FL3 vector (5' site CACTGTTG, 3' site CACCATG); XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumi Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTCCTAAAGCTCG and 3' end primer CGACCTGAGCTGAGGCCA."	
BASE COUNT	230 a 219 c 172 g 187 t 8 others

RESULT 8

A119218 LOCUS All19218 816 bp mRNA linear EST 02-SEP-1998 DEFINITION ue94h02.y1 Sugano mouse embryo mRNA clone IMAGE:149803 5' similar to sp: X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE); mRNA sequence.

ACCESSION All19218 VERSION All19218.1 GI:3519542

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 816)

AUTHORS Marr,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheibenbogen,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterton,R.

TITLE The WashU-HMM Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M.Mouse

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is royalty-free through LINL; contact the IMAGE consortium (info@image.llnl.gov) for further information.

RESULT 9

FEATURES	source
MGI: 936407	
Sed primer: custom primer used	
High Quality sequence stop: 473.	
Location/Qualifiers	
1. .815	
/organism="Mus musculus"	
/strain="C57BL"	
/db_xref="taxon:10090"	
/clone="IMAGE:1498803"	
/dev_stage="embryo, 14 dpc"	
/lab_host="DH10B;"	
/note="Vector: PM18S-FL3; Site_1: DraIII (CACTGTTG); Site_2: DraIII (CACCTATG); 1st strand cDNA was primed with an oligo(dt) primer (ATGGCCCTTTCCTTTCCTT); double stranded cDNA was ligated to a DraIII (TGTGGCCATCGG) digested and cloned into distinct DraIII sites of the PME18S-FL3 vector (5' site CACTGTTG, 3' site CACCATG); XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumi Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTCGTCCTAAAGCTCG and 3' end primer CGACCTGAGCTGAGGCCA."	
BASE COUNT	230 a 219 c 172 g 187 t 8 others

RESULT 8

A119218 LOCUS All19218 816 bp mRNA linear EST 02-SEP-1998 DEFINITION ue94h02.y1 Sugano mouse embryo mRNA clone IMAGE:149803 5' similar to sp: X04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE); mRNA sequence.

ACCESSION All19218 VERSION All19218.1 GI:3519542

KEYWORDS EST.

SOURCE house mouse.

ORGANISM Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 816)

AUTHORS Marr,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Scheibenbogen,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wyllie,T., Lennon,G., Soares,B., Wilson,R. and Waterton,R.

TITLE The WashU-HMM Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M.Mouse

Washington University School of Medicine

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is royalty-free through LINL; contact the IMAGE consortium (info@image.llnl.gov) for further information.

SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NIH-MGC http://mgc.ncbi.nlm.nih.gov/
AUTHORS	1 (bases 1 to 594)
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
JOURNAL	Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
COMMENT	Tissue Procurement: Jeffrey E. Green, M.D.; DNA library preparation: Life Technologies, Inc. DNA library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution found through the I.M.A.G.E. Consortium/LLNL at: http://ImageLLNL.gov Plate: LIAM927 row: P column: 08
FEATURES	High quality sequence stop: 589.
source	Location/Qualifiers
1.	594 <organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone_id="NCI_CGAP_L19" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: liver; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally; Primer: Oligo dT. Average Insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP library." ORIGIN BASE COUNT 175 a 162 c 142 g 115 t
Query Match	58.7%; Score 303 6; DB 12; Length 594;
Best Local Similarity	80.7%; Pred. No. 3e-70; Mismatches 394; Conservative 0; Indels 10; Gaps 3; Matches 16
Qy	16 TCGGGCTGAGCTGTGGATCTCTCAGTCGTTGAGACAGGGCTTATTC 75
Db	107 TCGGGCTGAGCTGTGGATCTCTCAGTCGTTGAGACAGGGCTTATTC 166
Qy	76 AACAAAGCCAGAGGTAGGTCACAGGGGCGCCACACGGATGGAT 135
Db	167 AACAAAGCCAGAGGTAGGTCACAGGGGCGCCACACGGATGGAT 226
Qy	136 GAGTGCGCTCGGAGCTGAGATCAAGAGGGCTGAGATGTTGCGAACCCOTCAAG 195
Db	227 GAGTGCGCTCGGAGCTGAGATGTTGCGAACCCOTCAAG 285
Qy	196 CCGGCCAAGTAGCTGCTGCTGCTGCCAGCAGCACAGCATGCCAG 255
Db	287 CCTACAAAGAACGCCCTCTACCGCCGCGCACACTGACATGCCAGACTCAG 346
Qy	256 RAGTATCAGCCCATCTACCAACAGAACCGAACAGCTCA -- GAGAAGGAAG 312
Db	347 AAGTCCCCGTCTATGACACACAGTAGGGAGTCGGGAAACAGAACTACAGGTGA-GAGA 406
Qy	313 AGATTGAGAACACAGTAGGGAGTCGGGAAACAGAACTACAGGTGA-GAGA 371
Db	407 ACATTCATGACACAGTAGGGAGTCGGGAAACAGAACTACAGGTGA-GAGA 466
Qy	372 CCCTCTGAGAGTAGGAGAACGCCAGCGCAGACCTTGCTCCACAGTAC 431
Db	467 GCCTCCCACGCGAGCAAAATGCCACATCACCGCAGATCTTGTGCTGASCAACT 526
Qy	432 TGAATGATGGATAACGGGCA-----AAATAATGTTGATACATTCAGATGG 485
Db	527 GCAAACATGGAACACTACAAATAACAATAATAGTCCTAAATACATTCAGAAGATGG 586
Qy	486 CATTGCC 493
Db	587 GCATTGCC 594
FEATURES	source
1.	594 <organism="Mus musculus" /strain="FVB/N" /db_xref="taxon:10090" /clone_id="NCI_CGAP_L19" /lab_host="DH10B (T1 phage-resistant)" /note="Organ: liver; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally; Primer: Oligo dT. Average Insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP library." ORIGIN BASE COUNT 175 a 162 c 142 g 115 t
Query Match	58.0%; Score 299 8; DB 9; Length 527;
Best Local Similarity	85.5%; Pred. No. 3.9e-78; Mismatches 413; Conservative 0; Indels 17; Gaps 5; Matches 39
Qy	99 TCTTCAGTCTGCTGAGACAGGGTTATTCAACAGCCACAGGGTATGGCTC 98
Db	527 TCTTCAGTCTGCTGAGACAGGGTTATTCAACAGCCACAGGGTATGGCTC 468
Qy	99 CAGCGTCCGAGGGGCCCTCAGACAGGGCATGCGTGTGATAGTGCGCTGCTGGAGCTGTGA 158
Db	467 CAGCGTCCGAGGGGCCCTCAGACAGGGCATGCGTGTGATAGTGCGCTGCTGGAGCTGTGA 408
Qy	159 TCTTGGGGCTGAGAGTAGTCGGGCCCTCAAGCTGCCAGTACGCTGCTGT 218
Db	407 TCTAAGGAGCTGGAGATGATGTCGCAAGCTGCTGCTGTGCTGCTGT 348
Qy	219 CGCGCCACGCCACAGGACATGCCAGAGCAAGCCAGAGTATGCCCTACCAA 278
Db	347 CGTGCACGCCACGCCACAGGACATGCCAGAGCAAGCCAGAGTATGCCCTACCAA 311
Qy	279 CAAGACAGGAGTCAGAGAAGGAAGGAAGTACATTTGAAAGACCAAGTAGAGGA 338
Db	310 -----ANGAAGTACATTTGAAAGAACCAGCAAGTGGAG 277

	BASE COUNT	127	a	154	c	175	g	185	t	1 others
QY	398	GCCACCGCAGGACCTTGTCTGCAGGTTACTGTAATGGCAAGAGGAC	397							
Db	276	GTGAGGAAACAGAAGTACAGGATGAGGAACCTCTGAGGAGTAA	217							
QY	156	AATATAGTTGATACATTAANGATGGCGTTCGGCCATGAAATACACAGTAA	97							
QY	515	CAT	517							
Db	96	CAT	94							
RESULT 11										
A187493/c	AT87493	Mus musculus	642	bp	mRNA	linear	EST	21-JUL-1999		
DEFINITION	u159b10x1 Sugano mouse liver mla	Mus musculus	cDNA clone							
IMAGE:1924219	3'	similar to gb:X57025	mRNA INSULIN-LIKE GROWTH							
FACTOR	Precursor (HUMAN)	gb:X04482	Mouse mRNA for							
ACCESSION	A187493	Proinsulin-like growth factor IB (MOUSE);	mRNA sequence.							
VERSION	A187493.1	GI:5550542	EST.							
SOURCE	Mus musculus	house mouse.								
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.									
REFERENCE	1 (bases 1 to 642)									
AUTHORS	Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Stobie, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swiller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Watsonson, R., and Wilson, R.									
TITLE	The WashU-NCI Mouse EST Project	1999								
JOURNAL	Unpublished (1999)									
COMMENT	Contact: Marra M/WashU-NCI Mouse EST Project	1999								
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA										
Fax:	314 286 1800									
Email:	mouseest@wustl.edu									
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.	MGI:980511									
Seq primer: custom primer used										
High quality sequence stop:	257.									
FEATURES	source									
/organism="Mus musculus"										
/strain="C57BL"										
/strain="C57BL"										
/db_xref="taxon:10090"										
/clone="IMAGE:1924219"										
/clone.lib="Sugano mouse liver mla"										
/sex="female"										
/dev_stage="adult"										
/lab_host="DH10B"										
/note="organ: liver; vector: PME18S-FL3; Site:1: Braili (CATCTGTC); Site:2: DraIII (CACCATGG); 1st strand cDNA was primed with an oligo(dT) primer										
[ATGCGGCCGTTGTTGTTGTT]; double stranded cDNA was ligated to a Braili adaptor [TCCTGGCTTCTGG], digested and cloned into distinct Braili sites of the PME18S-FL3 vector (5' site CATCTGTC, 3' site CACCATGG). XbaI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTCTGCTCTAAACCTGG and 3' end primer CGACCTGAGCTCGACACA."										
QY	9704477	Fax: 301 443 9890								
COMMENT	Chin, H	Email: MAST@mail.nih.gov								
JOURNAL	Genome Res. 6 (9), 791-806 (1996)	The sequence contained an oligo-dT track that was present in the oligonucleotide that was used to prime the synthesis of first strand cDNA and therefore this may represent a bona fide poly A tail. The sequence tag present in the cDNA between the NotI site								
MEDLINE	9704477									
COMMENT	National Institute of Mental Health, MSC 9643, Bethesda, MD 20892-6033, USA									
JOURNAL	Tel: 301 443 1706									
MEDLINE										
COMMENT										
JOURNAL										
MEDLINE										
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Page 9

and the oligo-dT track served to identify it as a clone from the normalized Pineal Glands library. cDNA Library Preparation: M. J. Soares Lab Clone distribution: Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It should be noted that Bento Soares is generating a small number of additional specialized non-redundant arrays of BMAP cDNAs whose availability will be considered under appropriate and limited collaborative arrangements.

FEATURES	POLYA=Yes.
Source	Location/Qualifiers
	I. 499
	/organism="Mus musculus"
	/protein_id="P02368"
	/taxon_id="10090"

QY	347	AACAGAACTACAGGATGA-GRAGACCTCTGTGAGAAGAGACGGCCACCGC	405
	199	AACRAGACCTACAGAATGAGGAGCCTCCACGGCAGAAATGCCACATCACCGC	140
QY	406	AGCACCTTGTCTGCACAGTACCGTAACATGGAACTCCGGCA-----AAA	459
	139	AGGACTCTTGTGCTGTCAGCACCTGCAAACATGCCAACACTACCAATAACATA	80
QY	460	TAAGTTGATCACATCAGAAT-GGCATTCCCCAATGAAATCAGCATACAT	517
	79	TAAGTCCATAAAATTAGAAAGATGGSCATTTCCCAGAATATAACAAGTAAACAT	21

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</ab_xref>"taxon:10990"
/clone="U1-M-BH3-Subg-M-11-0-UI"
/clone_1db="NIH_BMAP_M_S4"
/dev_stage="27-32 days"
/lab_host="DH10B (Life Technologies)"
/note="Vector: PT73D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The
NIH_BMAP_M_S4 library is a subtracted library of a series,
ultimately derived from a mixture of individually tagged,
normalized libraries from ten regions of the mouse brain
(cerebellum, brain stems, olfactory bulbs, hypothalamus,
cortex, amygdala, basal ganglia, pineal gland, striatum,
hippocampus) after a series of subtractions to reduce the
representation of cDNAs from which ESTs had already been
generated. The following serially subtracted libraries
were generated in this process: NIH_BMAP_M_S4,
NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, NIH_BMAP_M_S3_1,
NIH_BMAP_M_S2, NIH_BMAP_M_S1. The subtracted library
(NIH_BMAP_M_S4) was constructed as follows: PCR amplified
cDNA inserts from NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, and
NIH_BMAP_M_S3_1 clones from which 3' ESTs had been derived
was used as a driver in a hybridization with a pool of
the NIH_BMAP_M_S3_3, NIH_BMAP_M_S3_2, and NIH_BMAP_M_S3_1
libraries in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library)
was purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (LifeTechnologies) to generate the
NIH_BMAP_M_S4 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research
6:791-806, 1996)
TAG_LB=NIH_BMAP_M_S4
TAG_TISSUE=pineal-glands
TAG_SEQ=CAGAC

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AI169770/c	AI169770	468 bp	mRNA	linear	EST	20-JAN-1999
LOCUS	EST255669	Normalized rat liver, Bento Soares	Rattus sp.	cdna clone		
DEFINITION		RLIA07 3'	end,	mRNA sequence.		
ACCESSION	AI169770	AI169770.1	GI:3709810			
VERSION						
KEYWORDS						
SOURCE		Rattus sp.				
ORGANISM	Rattus sp.					
REFERENCE	Rattus					
AUTHORS	I. (bases 1 to 458)					
TITLE	Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D.					
JOURNAL	Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat Gene Index					
COMMENT	Unpublished (1998)					
OTHER_ESTS	TC50779					
CONTACT	Lee, NH					
THE INSTITUTE FOR GENOMIC RESEARCH						
9712, Medical Center Drive, Rockville, MD 20850, USA.						
TEL:	(301)-838-3529					
FAX:	(301)-838-0208					
EMAIL:	nhi@egg.org					
SEQ PRIMER	M13-21.					
FEATURES	Location/Qualifiers					
SOURCE	1..468					
ORGANISM	Rattus sp.					
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NOTE	/note="Organ: Liver; Vector: pR7r3pac; Site_1: EORI; Site_2: NOTI"					
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Best Local Similarity	80.5%	Pred. No. 4	5e-71;			
Matches	375;	Conservative	0;	Mismatches 80;	Indels 11;	Gaps 4;
QY	63 GGGCTTTATTCAACAGGCCAGGGTATGGCTCCAGCAGTCGGAGGGCCCTCGAC	122				
DB	468 GGGCTTATTCAACAGGCCAGGGTATGGCTCCAGCAGTCGGAGGGCCACACAGAC	409				
QY	123 AGGCATCGGAGGAGTGCTGCTCCAGCTGTGACTTAAGGAGCTGGATGATG 182					
DB	408 GGGCATGGTGGATGAGTGTGCTCCGGAGCTGATCTGGAGGGTGGAGTGACTG	349				
QY	183 CGCACCCCAAGGCCAGCTGAGCTGAGCTGCTGGCCAGGCCACACGACAT	242				
DB	348 TGCCTCGCTGAAGCTTACAAGTCAGCCCCCTACACAGAGAACAGAACGCTCA-	289	-GAG	299		
QY	243 GCCAAGACCAAGAGATATCAGCCCCCTACACAGAGAACAGAACGCTCA-	288	-GAG	229		
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QY 300 AKGGAAGGAGTACATTTGAGAACACAATAGAGGGASTGCAGGAAACAGAACTACA 359
 Db 228 TAAAGGAAGGAGTACACTTGAGAACACAAGTAGAGGAAGTCAGGAGCAGAACAGCTACA 169
 QY 360 GGTGTA-GAGACCCCTCTAGGAGTGAAGAAGGAGGCCAGGCCAGGCCCTTGCT 418
 Db 168 GAATGTTAGGAGGCCCTCCAGGAACAGAAATGGCACCGTACGCCAGTCCTTGCT 109
 QY 419 CTGCACAGTTACCTGTAACCTGGATACCGGCA---AAATACTGATCAC 472
 Db 108 GCTGTGAGCAACCTGCAAACATGGAAACCTGGCCAAATATCATATGAGTCATAC 49
 QY 473 ATTCAAGAGT-GGCATTCCCCAATGAATAACAGAGTACAT 517
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 A1604642
 LOCUS A1604642 882 bp mRNA linear EST 21-APR-1999
 DEFINITION vmp4308.y1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA
 Clone IMAGE:1001075, similar to gb:M11568 INSULIN-LIKE GROWTH
 FACTOR IB PRECURSOR (HUMAN); gb:X01282 Mouse mRNA for
 preproinsulin like growth factor IB (MOUSE); mRNA sequence.
 ACCESSION A1604642
 VERSION A1604642.1
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 882)
 Marr,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Stepcoski,W., Theising,B., Allen,M., Bowers,Y., Person
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Watson,R. and Wilson,R.
 The WashU-NCI Mouse EST Project 1999
 TITLE
 JOURNAL
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LInL ; contact the
 IMAGE Consortium (info@image.lnl.gov) for further information.
 MG:1565223
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 Seq Primer: -40RP from Gibco
 High quality sequence stop: 361.
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 Best Local Similarity 75.6%; Pred. No. 1.6e-70;

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 Db 377 GGACAGAGACCCCTTGCGNGCTGAGTTGTTGGATGTCAGTCGTTGGACCG 436
 QY 61 AGGGCTTATTCAACAGCCACAGAAATGGCACCGTACGCCAGTCCTTGCT 120
 Db 437 AGGGCTTATTCAACAGCCACAGCTATGGCTCAGATTCAGGGACCCAG 496
 QY 121 ACAGSCATCTGGTGAAGTGTCTGGTGTGTCAGGAGCTGGATGAT 180
 Db 497 ACAGGCATGTGGTGAAGTGTCTGGTGTGTCAGGAGCTGGATGAT 556
 QY 181 TGCCGACCCCTCAAGCCCTCAACTCACTCGCTGTGCGGCCAGCCACCGAC 240
 Db 557 TGTGCCCACTGAAAGCCATCANAAGCAGCCGCCCTATCGTGCCTCACGCCAGCACGAC 616
 QY 241 ATGCCAAGGCCAGAATGATCAGCCCATCTAACACAGAACAGCTCACAG- 299
 Db 617 ATGCNNAGCTCAGAATGCCCTNCTATCGACNNACAGAACAGCTGCAAG 576
 QY 300 -AAGGAAGGAGTACATTGAAGAACAAAGTAGAGGAGGAGCAGAACATA 357
 Db 677 GAGAGGAAGGGAGTACATTGGAGAACACANGTGAGGAAAGTCAGCTA 736
 QY 358 CAGGATGAGAACCCCTGTGAGGAGGAGAGGAGGAGGACCGCTTG 417
 Db 737 CCAGATGTAGGAGGCT-TCAACCGAGCAGAACATACCCAGNAGACAGCTTG 795
 QY 418 TGTGCAAGTACCTGAGTACCTGGAGCCACGAGCTTACCAATTAAAGTGTAC 473
 Db 796 T-GCTGTGAGCTACGCCAACATGCCAACCTTACCAATTAAAGTGTAC 854
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 similar to gb:X50251.mna1 INSULIN-LIKE GROWTH FACTOR IA PRECURSOR
 (HUMAN); mRNA sequence.
 ACCESSION A1478804
 VERSION A1478804.1
 KEYWORDS EST.
 SOURCE
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 430)
 REFERENCE
 AUTHORS
 TITLE
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lemon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone Distribution: NCI-CGAP clone distribution information can be
 found through the NCI-CGAP Consortium/LInL at:
 www.bio.lnl.gov/DbRp/Image/image.html
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plasmid DNA from the normalized library NCI_CGAP_Kid3 was
prepared and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtraction
hybridization reaction. The driver was PCR-amplified clones
from a pool of 5,000 clones made from the same library
(clones 132376-132391, 145607-145675, and
150052-1502855). Subtraction by Bento Soares and M.
Fatima Bonaldo." subtraction by Bento Soares and M.

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BASE COUNT	96 a	93 c	103 g	138 t
ORIGIN				

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				Gaps 4;
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Qy	424	C-AGTTACCTG-TAACATGGANTACCGCCAAAATTAAGTTGATCACATTCAAG	481	
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